

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:11 ; Search time 172 Seconds
(without alignments)
6118.119 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctataggcgcgcgtgtgtcg.....gccctgcggagccgcacg 592

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *

- 1: /cgm2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgm2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgm2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgm2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgm2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgm2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgm2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	52.4	982	3	US-08-725-532A-4
2	310	52.4	982	3	US-09-016-434-993
3	234	39.5	1315	3	US-09-164-193-1
4	234	39.5	1315	3	US-09-221-448A-1
5	52.8	8.9	7218	2	US-08-232-463-14
6	45.2	7.6	22118	3	US-09-815-981A-5
7	44.6	7.5	614	3	US-09-902-540-1318
8	42.4	7.2	1732	3	US-09-270-767-2595
9	42.4	7.2	1732	3	US-09-270-767-17877
10	41.8	7.1	601	3	US-09-949-016-142965
11	41.8	7.1	601	3	US-09-949-016-142966
12	41.8	7.1	601	3	US-09-949-016-142967
13	41.8	7.1	265038	3	US-09-949-016-15779
14	41.6	7.0	1696	3	US-09-835-811-1
15	41.4	7.0	290	3	US-10-131-827-8418
16	41	6.9	612	3	US-09-902-540-1357
17	40.8	6.9	2744	3	US-09-071-101-1
18	40.8	6.9	2744	3	US-09-369-618-1
19	40.8	6.9	2744	3	US-09-369-617-1
20	40.6	6.9	2447	2	US-09-014-969-14
21	40.2	6.8	1030	3	US-09-945-376-3
22	40	6.8	555	3	US-08-905-223-37
23	40	6.8	555	3	US-09-247-155-37
24	40	6.8	555	3	US-09-599-360B-23

25 40 6.8 3 US-09-663-600A-37 Sequence 37, Appl
26 40 6.8 3 US-09-621-976-23 Sequence 23, Appl
27 40 6.8 3 US-09-513-999C-23 Sequence 23, Appl
28 40 6.8 3 US-09-471-276-23 Sequence 23, Appl
29 40 6.8 3 US-09-903-190-37 Sequence 37, Appl
30 39.8 6.7 1039 3 US-09-902-540-1280 Sequence 1280, Ap
31 39.6 6.7 6078 3 US-09-173-914-1 Sequence 1, Appl
32 39.4 6.7 505 3 US-09-621-976-15639 Sequence 15639, A
33 39.2 6.6 411 3 US-09-598-401C-30 Sequence 30, Appl
34 39.2 6.6 2791 3 US-09-570-367C-1 Sequence 1, Appl
35 39.2 6.6 2791 3 US-09-915-524-1 Sequence 1, Appl
36 39.2 6.6 2791 3 US-09-934-634-1 Sequence 1, Appl
37 39.2 6.6 2791 3 US-09-917-278-1 Sequence 1, Appl
38 39 6.6 2240 3 US-09-814-351-6 Sequence 6, Appl
39 39 6.6 2240 3 US-09-814-292-1 Sequence 1, Appl
40 39 6.6 2240 3 US-09-814-357-6 Sequence 6, Appl
41 39 6.6 6755 3 US-08-931-999-4 Sequence 4, Appl
42 38.8 6.6 382 3 US-09-598-401C-39 Sequence 39, Appl
43 38.8 6.6 515 3 US-09-598-401C-84 Sequence 84, Appl
44 38.8 6.6 2571 3 US-09-598-401C-93 Sequence 93, Appl
45 38.4 6.5 1484 3 US-09-991-181-232 Sequence 232, Appl

ALIGNMENTS

RESULT 1
US-08-725-532A-4
; Sequence 4, Application US/08725532A
; Patent No. 6020179
; GENERAL INFORMATION:
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,532A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0130 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-08-725-532A-4
Query Match 52.4%; Score 310; DB 3; Length 982;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;

BEST AVAILABLE COPY

Query Match	7.6%	Score 45.2;	DB 3;	Length 22118;
Best Local Similarity	52.7%;	Pred. No. 0.031;		
Matches 98; Conservative	0;	Mismatches 88;	Indels 0;	Gaps 0;
Qy	192	TTTGAGTTTTAAAGTTTCTTCCTGAGCTTTTTTGGTTGTTCTTTTTATTTTTTGGCCTC	251	
Db	19801	TTTGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT	19860	
Qy	252	TTTATAGCTATACCGACTCTGAGAGACGGAGTTTGAGTTGCCCGCTTACCTTGCTGG	311	
Db	19861	TTTGTGTGTTGTTGTGTTGTGTTGTGCTGGGTTGGGTTGGGTTGGGTTGG	19920	
Qy	312	GTGTGGGGGGGGCGCGGGCTGTTTTCCTTTCTTTTTTAAAGAGTTGGGTTTCTTTT	371	
Db	19921	GTTGGGTTGGGTTGGGTTGTGTTGTTTGGTTTGTGTTGTTGTTGTTGTTGTTT	19980	
Qy	372	TTAATT	377	
Db	19981	TTGTTT	19986	

RESULT 7
US-09-902-540-1318/c
; Sequence 1318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1318
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(614)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318

Query Match	7.5%;	Score 44.6;	DB 3;	Length 614;
Best Local Similarity	52.4%;	Pred. NO. 0.011;		
Matches 98;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;
Qy	187	TTCACTTTGAGTTTTTAAGTTTTCTTCGTCGAGCTTTTTTGGTTGTTCTTTTATATTTTT	246	
Db	462	TTTTTTTTTTTTTTGGTT	403	
Qy	247	GCCTCTTTATGACTATATCCAGCTCTGAGAGACGGAGTTTGAGATTGCCCGCTTACITTG	306	
Db	402	TTCTTTTTTTTTTTTGTATTATGTTTTTTTGTGTGTGTTTTTTTGTTTTTTTTATTTT	343	
Qy	307	GTTCGGTTTGGGGGGCGCGGCTGTTTTGTTCCTTTTCTTTTAAAGAGTTGGGTTTT	366	
Db	342	GTTTTTGTTTTGTTTTTTTTTTGTCTTTCTTTTCTTTTGTGTTGTTTGTCTT	283	
Qy	367	CTTTTTT	373	
Db	282	TTTTTTT	276	

RESULT 8
US-09-270-767-2595/c
; Sequence 2595, Application US/09270767
; Patent No.6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: patentIn Ver. 2.0
; SEQ ID NO 2595
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-2595

Query Match          7.2%; Score 42.4; DB 3; Length 1732;
Best Local Similarity 50.5%; Pred. No. 0.068;
Matches 103; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 180  GCGCGGGTTCACCTTTGAGTTTTAAAGTTTTCTTTGCTGAGACCTTTTTGGTGTGTTCTTTTT 239
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 240  ATTTTTTGCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTT 299
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 494  TTTTITTTGTAATTCGAATTTTGTACGCTATTTATGAATTTACATTCAATTCATTGCTA 435
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 300  TACTTTGGTTGGGTTGGGGGGCGGGCGCTCTTTTGTTCCTTTCTTTTTTAAGAGTT 359
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 434  TGCTTCGTTGATTTGGGTTTTATGATTTTTTTTTTTCGTTTTTTTTTAAATGTAATAATTT 375
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 360  GGGTTTTCTTTTTTAATATATCCAA 383
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 374  TTTTTCGGTTTTGCTTTTGTATAA 351
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9
US-09-270-767-17877/c
; Sequence 17877, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17877
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17877

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	Query Match	7.2%;	Score 42.4;	DB 3;	Length 1732;
	Best Local Similarity	50.5%;	Pred. No. 0.068;		
	Matches 103;	Conservative	0;	Mismatches 101;	Indels 0; Gaps 0;
Qy	180	GGCGGGTTCACATTTGAGTTTTTAAAGTTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTT	239		
Db	554	GGCTGTTTTACATTTAAAGTTTCTCTTTTTTACAGTTTCGTTTTTGGGGTTTCTTTAT	495		
Qy	240	ATTTTGGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTTGC CGGTT	299		
Db	494	TTTTTTTGTATTTTCGATTTTTTGTACGCTATTTATGAAATTTACTTTGAAATTTCA	435		
Qy	300	TACTTTTGTTTGGTTGGGGGGGGCGGCGCTGTTTGTTCCTTTTCTTTTTTAAAGAGTT	359		
Db	434	TGCTTCGTTTGAATTTGGGTTTATGATTTTTTTTTTTCGGTTTTTTTTTATTTGTAAAAATTT	375		
Qy	360	GGGTTTTCTTTTTTAAATATCCAA	383		
Db	374	TTTTTTCGGTTTTTGCTTTGTATAA	351		

RESULT 10
US-09-949-016-142965/c
; Sequence 142965, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142965
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142965

Query Match 7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066; 52; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 183 CGGGTTCACCTTGTAGTTTAAAGTTTCTTCTGAGCTTTTGGTGTCTTTTATT 242
Db 364 CGAGGACACTCTGAGTATCTGAGTTTGGTTGATAGCTTTTGTCTTTT 305
Qy 243 TTTTGGCTTTTATGACTATCCAGCTCTGAGAGCGGAGTTTGAGTTGCCGCTTTAC 302
Db 304 TTTTGACAAGGCTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGATCACAGTTTCC 245
Qy 303 TTTGG 307
Db 244 TGTAG 240

RESULT 11
US-09-949-016-142966/c
; Sequence 142966, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142966
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142966

Query Match 7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066; 52; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 183 CGGGTTCACCTTGTAGTTTAAAGTTTCTTCTGAGCTTTTGGTGTCTTTTATT 242

Db 585 CGAGGACACTCTGAGTATCTGAGTTTGGTTGATAGCTTTTGTCTTTT 526
Qy 243 TTTTGGCTTTTATGACTATCCAGCTCTGAGAGCGGAGTTTGAGTTGCCGCTTTAC 302
Db 525 TTTTGACAAGGCTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGATCACAGTTTCC 466
Qy 303 TTTGG 307
Db 465 TGTAG 461

RESULT 12
US-09-949-016-142967/c
; Sequence 142967, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142967
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142967

Query Match 7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066; 52; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 183 CGGGTTCACCTTGTAGTTTAAAGTTTCTTCTGAGCTTTTGGTGTCTTTTATT 242
Db 589 CGAGGACACTCTGAGTATCTGAGTTTGGTTGATAGCTTTTGTCTTTT 530
Qy 243 TTTTGGCTTTTATGACTATCCAGCTCTGAGAGCGGAGTTTGAGTTGCCGCTTTAC 302
Db 529 TTTTGACAAGGCTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGATCACAGTTTCC 470
Qy 303 TTTGG 307
Db 469 TGTAG 465

RESULT 13
US-09-949-016-15779
; Sequence 15779, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15779
; LENGTH: 265038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(265038)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15779

Query Match
Best Local Similarity 7.1%; Score 41.8; DB 3; Length 265038;
Matches 73; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 183 CGGCTTACATTTGAGTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTATT 242
DB 129123 CGAGGACACTCTGAGTATCTGAGTTGGTTGATTAGCTTTTTTTTTTTTT 129182
QY 243 TTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTTAC 302
DB 129183 TTTTGACAGGCTCTGGCTCTGCCATTGAGCTGTAGATAGTGGGGATCAGATTAC 129242
QY 303 TTTGG 307
DB 129243 TGTAG 129247

RESULT 14
US-09-835-811-1/c
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match
Best Local Similarity 7.0%; Score 41.6; DB 3; Length 1696;
Matches 98; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 198 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 257
DB 1692 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 1633
QY 258 ACTATCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTACTTTGGTTGGG 317
DB 1632 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 1573
QY 318 GGGGGGGGGGCTTTTGTGTTCTTTTAAAGTTTGGTTTCTTTTAAATTTT 377
DB 1572 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 1513
QY 378 ATCCAAACAGTG 389
DB 1512 ATCTATACAGTG 1501

RESULT 15
US-10-131-827-8418
; Sequence 8418, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8418
; LENGTH: 290
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8418

Query Match
Best Local Similarity 7.0%; Score 41.4; DB 3; Length 290;
Matches 99; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 199 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 258
DB 1 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 60
QY 259 CTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGG 318
DB 61 TTTTAAAGTTTCTTGTGAGCTTTTGTGTTCTTTTAAATTTTTCCTTTTATG 120
QY 319 GGGGGGGGGGCTTTTGTGTTCTTTTAAAGTTTGGTTTCTTTTAAATTTTTCCTTTTATG 378
DB 121 GGGGGGGGGGCTTTTGTGTTCTTTTAAAGTTTGGTTTCTTTTAAATTTTTCCTTTTATG 180
QY 379 TCCAAACAGTG 393
DB 181 TCCAAACAGTG 195

Search completed: April 3, 2006, 05:42:46
Job time : 173 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:30 ; Search time 3204 Seconds
(without alignments)
10502.910 Million cell updates/sec

Title: US-10-624-670-1

Perfect score: 592

Sequence: 1 ctatagggcagcgtggtcg.....gcccgtagggcgcccatg 592

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	557	94.1	2850	6	AX393317	Sequence
2	557	94.1	46561	8	AP005888	Homo sapi
3	557	94.1	141371	8	AP005792	Homo sapi
4	557	94.1	152418	8	AC100803	Homo sapi
5	546	92.2	77656	14	AC138743	Homo sapi
6	337	56.9	1329	8	BC003105	Homo sapi
7	337	56.9	1396	6	C0827376	Sequence
8	310	52.4	982	6	AB270430	Sequence
9	310	52.4	982	6	BD003637	Disease a
10	240	40.5	572	6	C0716903	Sequence
11	240	40.5	572	6	C0718557	Sequence
12	240	40.5	1006	6	CS113117	Sequence
13	240	40.5	1006	8	AF041434	Homo sapi
14	234	39.5	1315	6	AR162252	Sequence
15	226	38.2	963	8	HS427654	Homo sapi
16	141.4	23.9	315395	14	AC132017	Rattus no
17	131.4	22.2	2291	9	BC066043	Mus muscu
18	131.4	22.2	168400	9	AC119884	Mus muscu

19	84.2	14.2	232503	14	AC098900	Rattus no
20	64.8	10.9	817	9	AF035645	Mus muscu
21	54.2	9.2	162934	14	AC139448	Rattus no
22	52.8	8.9	7218	6	I66494	Sequence 14
23	52	8.8	7758	6	AX346005	Sequence
24	51.6	8.7	73989	14	AC101573	Mus muscu
25	51.6	8.7	213524	14	AC073339	Homo sapi
26	51.2	8.6	226454	14	AC162820	Bob tauru
27	50.8	8.6	7698	6	AX346602	Sequence
28	50.8	8.6	167991	9	AC125175	Mus muscu
29	50.8	8.6	213272	14	AC135668	Mus muscu
30	50	8.4	47722	14	AC113140	Homo sapi
31	49.4	8.3	127955	14	AC139907	Rattus no
32	49	8.3	202083	14	AC023833	Mus muscu
33	48.8	8.2	877	8	HS425386	Homo sapi
34	48.8	8.2	7721	6	CS105998	Sequence
35	48.8	8.2	83296	14	AC022588	Homo sapi
36	48.8	8.2	120644	14	AC026496	Homo sapi
37	48.6	8.2	4374	6	CS124658	Sequence
38	48.6	8.2	5203	6	C0807142	Sequence
39	48.6	8.2	5203	6	AX795920	Sequence
40	48.6	8.2	5203	6	AX822442	Sequence
41	48.6	8.2	5203	6	AX826082	Sequence
42	48.6	8.2	71532	14	AC023655	Homo sapi
43	48.6	8.2	88712	14	AC097315	Mus muscu
44	48.6	8.2	349980	6	AX344556	Sequence
45	48.4	8.2	173854	14	AC073047	Homo sapi

ALIGNMENTS

RESULT 1
AX393317
LOCUS AX393317 2850 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 247 from Patent WO0210217.
ACCESSION AX393317
VERSION AX393317.1 GI:19701330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS St Croix, B., Kinzler, K.W. and Vogelstein, B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 247 07-FEB-2002;
The Johns Hopkins University (US)

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Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e-135;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 36 CTGAGTGGTTCAAGTTCATTTCTCTGGCCCTTGGGGGCTTGGGGCCACC 95
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Qy 96 TCTCAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCGGTGGG 155
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Qy 156 GTCCAGTCTGGGACACATCTTGGCGGGGGTTCACATTGAGTTTTTAAGTTCTTTTC 215
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Db      825  TGGGGACTTCTAGGTCGTGTCGCCAGCTTCTCTGAGTCCCTCTGCCCTGCCGGCC 884
Qy      576  CGTCGGGAGCGCCATG 592
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RESULT 2
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DEFINITION Homo sapiens genomic DNA, chromosome 8q24.3, clone: KB1897C9,
complete sequence.
ACCESSION AP005888
VERSION   AP005888.3 GI:25901050
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
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          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1
AUTHORS   Shimizu,N. and Asakawa,S.
TITLE     Homo sapiens DNA chromosome 8 SEQUENCE
JOURNAL   Published Only in Database (2002)
REFERENCE 2 (bases 1 to 46561)
AUTHORS   Shimizu,N. and Asakawa,S.
TITLE     Direct Submission
JOURNAL   Submitted (09-NOV-2002) Nobuyoshi Shimizu, Keio University, School
          of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
          160-8582, Japan (E-mail:nshimizu@db.med.keio.ac.jp,
          Tel:81-3-3351-2370, Fax:81-3-3351-2370)
COMMENT   On Nov 28, 2002 this sequence version replaced gi:25188175.
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Query Match      94.1%; Score 557; DB 8; Length 46561;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTGAGTTGGTTCAGTTCAAGTTCATTTCTCTCTGCGCCCTTGGGGGCTTGGGGGCCACC 95
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QY 576 CGTCGGAGGCGCCATG 592
DB 8939 CGTCGGAGGCGCCATG 8955
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RESULT 3

AP005792

LOCUS

DEFINITION

Homo sapiens genomic DNA, chromosome 8q24, clone: KB1533H12,

complete sequence.

ACCESSION

AP005792

VERSION

AP005792.5 GI:29170597

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

AUTHORS

TITLE

Shimizu,N. and Asakawa,S.
Homo sapiens DNA chromosome 8 SEQUENCE

JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 141371)
AUTHORS Shimizu.N. and Asakawa.S.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2002) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:nehimizu@db.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
COMMENT On Mar 24, 2003 this sequence version replaced gi:28971758.
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TITILE	Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
JOURNAL	Direct Submission
REFERENCE	Submitted (10-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	4 (bases 1 to 152418) Birren, B., Nusbaum, C., Lander, E., Abouelheil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, X., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., McEldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITILE	Direct Submission
JOURNAL	Submitted (20-MAY-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On May 20, 2003 this sequence version replaced gi:29501910. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L21447
Center clone name: 3064 M 3

Only the last 152.4 kilobases of this clone are being submitted. The remainder overlaps either accession number AC011676 [WICGR project I3081] or accession number AC138547 [WICGR project L29199]

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Query Match 94.1%; Score 557; DB 8; Length 152418;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 557; Conservative 0; Mismatches 0; Indels 0;

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SEQUENCE SAMPLING.
ACCESSION AC138743
VERSION AC138743.1 GI:27764716
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 77656)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP13-994N10
JOURNAL
REFERENCE
2 (bases 1 to 77656)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Canarata,J., Chang,J., Chazaro,B., Choepel,V., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,I., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
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Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (16-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WBR
Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L29168

Center Clone name: 994_N_10

* NOTE: This record contains 72 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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 complete cds.
 ACCESSION BC003105
 VERSION BC003105.1 GI:13111874
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 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1329)
 AUTHORS Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Krausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
 Altshuler, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
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 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
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 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalhus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1329)
 Strausberg, R.
 Direct Submission
 Submitted (13-FEB-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabh, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
 Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacques
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 DEFINITION Sequence 9 from Patent WO2004050117.
 ACCESSION CQ827376
 VERSION CQ827376.1 GI:49455856
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Meise, M., Eulenberger, K., Nguyen, T. and Tsentsenis, T.
 TITLE Proteins involved in the regulation of energy homeostasis
 JOURNAL Patent: WO 2004050117-A 9 17-JUN-2004;
 Develogen Aktiengesellschaft fuer entwicklungsbiologische Forschung
 (DE)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 2837 06-SEP-2002;
PE Corporation (NY) (US)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Corfe, B. and Chirakkal, H.
TITLE Gene screen
JOURNAL Patent: WO 2005054507-A 135 16-JUN-2005;
University of Sheffield (GB)
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Hominidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 4491 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 353 AAGAGTTGGGTTTCTTTTAAATATCAAAACAGTGGGAGCTTCTCTCCCCACACCCA 412
Db 1 AAGAGTTGGGTTTCTTTTAAATATCAAAACAGTGGGAGCTTCTCTCCCCACACCCA 60
QY 413 AGTATTGACAAATATTGTGCGGGGTATGCGGGGTGTTTAAATCTCGTTTCTCTTG 472
Db 61 AGTATTGACAAATATTGTGCGGGGTATGCGGGGTGTTTAAATCTCGTTTCTCTTG 120
QY 473 GACAAGCACAGGATCTCGTTCTCTCAATTTTGGGGGTGTGGGGACTTCTCAGGTC 532
Db 121 GACAAGCACAGGATCTCGTTCTCTCAATTTTGGGGGTGTGGGGACTTCTCAGGTC 180
QY 533 GTGTCCCGCAGCTTCTCTGAGTCCCTTCTGCGGCGCCGTCGGGAGGCCCATG 592
Db 181 GTGTCCCGCAGCTTCTCTGAGTCCCTTCTGCGGCGCCGTCGGGAGGCCCATG 240
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LOCUS AF041434 1006 bp mRNA linear PRI 09-AUG-1998
DEFINITION Homo sapiens potentially prenylated protein tyrosine phosphatase hPRL-3 mRNA, complete cds.
ACCESSION AF041434
VERSION AF041434.1 GI:3406429
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1006)
AUTHORS Zeng, Q., Tan, Y.H. and Hong, W.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1998) Membrane Biology Laboratory, Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore 117609, Singapore
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Best Local Similarity 100.0%; Pred. No. 3.5e-52;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 353 AAGAGTGGGTTTCTTTTAAATATCCAAACAGTGGGAGCTTCCTCCCCACACCA 412
DB 1 AAGAGTGGGTTTCTTTTAAATATCCAAACAGTGGGAGCTTCCTCCCCACACCA 60
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DB 61 AGTATTGCCAATATTGTGCGGGGTATGGGGTGGTGTAAATCTGTTCTCTTG 120
QY 473 GACAAGCACAGGAGTCTGTTCTCTCATTTTGGGGGTGTGGGGAGCTTCTCAGGTC 532
DB 121 GACAAGCACAGGAGTCTGTTCTCTCATTTTGGGGGTGTGGGGAGCTTCTCAGGTC 180
QY 533 GTGTCCCGAGCTTCTCTGCAAGTCCCTTCGCCCTGCGGGCCCGTGGGAGGCCCATG 592
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LOCUS AR162252 1315 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6258582.
ACCESSION AR162252
VERSION AR162252.1 GI:16229398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1315)
AUTHORS Acton, S.
TITLE CSATP nucleic acid molecules and uses therefor
JOURNAL Patent: US 6258582-A 1 10-JUL-2001;
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Best Local Similarity 100.0%; Pred. No. 1.3e-50;
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QY 479 CACAGGAGTCTGTTCTCTCTCATTTTGGGGGTGTGGGAGCTTCTCAGGTCGTGTC 538
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QY 539 CACAGCTTCTCTGCACTCCCTTCTGCGGGGCCGTCGGGAGGCCCATG 592
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HSA276554 963 bp mRNA linear PRI 15-DEC-2002
LOCUS Homo sapiens mRNA for protein tyrosine phosphatase hPRL-3, short form.
DEFINITION
ACCESSION AJ276554
VERSION AJ276554.1 GI:26985935
KEYWORDS hPRL-3 gene; protein tyrosine phosphatase hPRL-3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ievolella, C., Stanchi, F., Pacchioni, B., Silvia, T., Frigimelica, E., Scannapieco, P., Corso, V., Blasio, B. and Lanfranchi, G.
TITLE Full-length of some muscular transcripts, Telethon (Italy) project B41
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 963)
AUTHORS Ievolella, C.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-2000) Ievolella C., CRIBI Biotechnology Centre, Universita' di Padova, via G. Colombo 3, 35121, ITALY
COMMENT splice variant of AF041434.
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Query Match   38.2%; Score 226; DB 8; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.7e-48;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 427 ATTGTGCGGGGTATGGGGTGGGTTTAAATCTGTTTCTTGGACAAGCACAGGGA 486
Db 61 ATTGTGCGGGGTATGGGGTGGGTTTAAATCTGTTTCTTGGACAAGCACAGGGA 120

Qy 487 TCTGTTCTCTCATTATTTTGGGGGTGTGTGGGGACTTCTCAGGTGTTGTCGCCAGCCTT 546
Db 121 TCTGTTCTCTCATTATTTTGGGGGTGTGTGGGGACTTCTCAGGTGTTGTCGCCAGCCTT 180

Qy 547 CTCTGAGTCCCTTCTGCCCTGCCGCCCGTCCGGAGGCGCATG 592
Db 181 CTCTGAGTCCCTTCTGCCCTGCCGCCCGTCCGGAGGCGCATG 226

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Search completed: April 3, 2006, 06:43:42
Job time : 3210 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:33 ; Search time 3493 Seconds
(without alignments)
7929.560 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctataggcagcgtggtcg.....gccctggagggcccatg 592

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_ga81: *
10: gb_ga82: *
11: gb_ga83: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555.8	93.9	955	5	BX439784
2	555	93.8	1042	1	AL525371
3	555	93.8	1046	1	AL541981
4	545.6	92.2	1009	1	AL530939
5	545	92.1	956	1	AL542316
6	532.6	90.0	953	1	AL528298
7	527.6	89.1	954	1	AL550979
8	503.6	85.1	868	3	BI767860
9	502	84.8	706	8	CX759082
10	495.8	83.8	947	1	AL554544
11	484.2	81.8	932	3	BI771877
12	474.8	80.2	966	5	BU145820
13	453.6	76.6	904	1	AL549255
14	453.4	76.6	940	3	BI770311
15	450.8	76.1	861	3	BI834269
16	439.8	74.3	763	2	BI256315
17	398.8	67.4	1002	2	BI488596
18	388.6	67.3	889	1	AL528665
19	393.8	66.5	1077	6	CD251553
20	347.8	58.8	944	1	AL523466
21	337.4	55.3	329	7	CN368835
22	302.6	51.1	886	3	BI754659

23	302.4	51.1	671	3	BI765398
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25	291.6	49.3	1031	5	BQ881257
26	291.2	48.2	826	2	BF343031
27	286.2	48.3	900	2	BF342107
28	278.4	47.0	890	2	BE871184
29	274.4	46.4	671	3	BI489974
30	270	45.6	622	7	CR976547
31	267	45.1	542	7	CR981907
32	262.6	44.4	946	5	BQ883236
33	260.2	44.0	788	3	BI756422
34	253.4	42.8	474	2	BG003094
35	245.8	41.5	465	2	BG003036
36	240	40.5	462	1	AA454501
37	221	37.3	547	2	BE257755
38	211	35.6	647	3	BM791220
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40	198.2	33.5	1086	3	BM551642
41	196.8	33.2	729	7	CF994511
42	194	32.8	606	5	BQ638166
43	194	32.8	757	3	BM011663
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ALIGNMENTS

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LOCUS BX439784 Homo sapiens PLACENTA Homo sapiens cdna linear EST 04-MAY-2004
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX439784.2 GI:47003679
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 955)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30775779.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
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/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
Query Match 93.9%; Score 555.8; DB 5; Length 955;
Best Local Similarity 99.5%; Pred. No. 1.6e-130;
Matches 554; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 841 CGTCGGGAGGCGCCATG 857
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AL525371 1042 bp mRNA linear EST 24-MAR-2004
LOCUS
DEFINITION
AL525371 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION
AL525371
VERSION
AL525371.3 GI:45700569
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1. (bases 1 to 1042)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:31063235.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .1042
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/mol_type="mRNA"
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FEATURES
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match 93.8%; Score 555; DB 1; Length 1042;
Best Local Similarity 99.6%; Pred. No. 2.5e-130;
Matches 555; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 36 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 95
Db 303 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 362
QY 96 TCTGAGTGAAGGGGGCTGTCTGCGCCATCCCAATATGTGAGAGGGCCCGGCTGTGGG 155
Db 363 TCTGAGTGAAGGGGGCTGTCTGCGCCATCCCAATATGTGAGAGGGCCCGGCTGTGGG 422
QY 156 GTCCAGCTCTGACACACTGCTTGGGGGGGGGTTCACTTTGAGTTTTTAAGTTCTTTGC 215
Db 423 GTCCAGCTCTGACACACTGCTTGGGGGGGGGTTCACTTTGAGTTTTTAAGTTCTTTGC 482
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Db 843 CGTCGGGAGGCGCCATG 859

RESULT 3
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LOCUS
DEFINITION
AL541981 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YN08
ACCESSION
AL541981
VERSION
AL541981.3 GI:45717557
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1. (bases 1 to 1046)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30546679.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

FEATURES

source

ORIGIN

Query Match 93.8%; Score 555; DB 1; Length 1046;
Best Local Similarity 99.6%; Pred. No. 2.5e-130;
Matches 555; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 36 CTGGAGTTGGTTCAGTTCAGTTCATCTTCTCTGGCCCTTGGGGCTTGGGGCCACC 95
DB 303 CTGGAGTTGGTTCAGTTCAGTTCATCTTCTCTGGCCCTTGGGGCTTGGGGCCACC 362

QY 96 TCTGAGTGAAGGGGCTGTCGCCCATCCACCAATGTGGAGAGGGCGCCCGGTGGG 155
DB 363 TCTGAGTGAAGGGGCTGTCGCCCATCCACCAATGTGGAGAGGGCGCCCGGTGGG 422

QY 156 GTCCAGCTCTGACACTGTCTGGCGCGCGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 215
DB 423 GTCCAGCTCTGACACTGTCTGGCGCGCGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 482

QY 216 TGAGCTTTTGGTGTCTTTTAAATTTTGGCTTTTATGACTATCCAGCTCTGAGAG 275
DB 483 TGAGCTTTTGGTGTCTTTTAAATTTTGGCTTTTATGACTATCCAGCTCTGAGAG 542

QY 276 ACGGAGTTGAGTTGGCCCTTACCTTGGTGGGTGGGGGGGGCGGGCTGTT 335
DB 543 ACGGAGTTGAGTTGGCCCTTACCTTGGTGGGTGGGGGGGGCGGGCTGTT 602

QY 336 TGTTCCTTTTCTTTTAAAGTTGGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 215
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QY 396 TTCTCTCCCCACACCCCAAGTATTTGCACAAATTTTGTGCGGGGTATGGGGTGGT 455
DB 663 TTCTCTCCCCACACCCCAAGTATTTGCACAAATTTTGTGCGGGGTATGGGGTGGT 722

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DB 723 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCTCATTTTGGGGGTGTG 782

QY 516 TGGGAGCTTCTCAGGTGTCGCCAGCCTTCTGTCAGTCTCTTCTGCGCTTGGCGGCC 575
DB 783 TGGGAGCTTCTCAGGTGTCGCCAGCCTTCTGTCAGTCTCTTCTGCGCTTGGCGGCC 842

QY 576 CGTCGGGAGGGCCCATG 592
DB 843 CGTCGGGAGGGCCCATG 859

RESULT 4

AL530939

LOCUS

DEFINITION

AL530939 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
1009 bp mRNA linear EST 24-MAR-2004

cDNA clone CSODD003YN11 5-PRIME, mRNA sequence.

ACCESSION AL530939

VERSION AL530939.3 GI:45705888

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1009)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:31068772.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source

Location/Qualifiers

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 92.2%; Score 545.6; DB 1; Length 1009;
Best Local Similarity 99.6%; Pred. No. 6.3e-128;
Matches 556; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 36 CTGGAGTTGGTTCAGTTCAGTTCATCTTCTCTGGCCCTTGGGGCTTGGGGCCACC 95
DB 303 CTGGAGTTGGTTCAGTTCAGTTCATCTTCTCTGGCCCTTGGGGCTTGGGGCCACC 362

QY 96 TCTGAGTGAAGGGGCTGTCGCCCATCCACCAATGTGGAGAGGGCGCCCGGTGGG 155
DB 363 TCTGAGTGAAGGGGCTGTCGCCCATCCACCAATGTGGAGAGGGCGCCCGGTGGG 422

QY 156 GTCCAGCTCTGACACTGTCTGGCGCGCGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 215
DB 423 GTCCAGCTCTGACACTGTCTGGCGCGCGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 482

QY 216 TGAGCTTTTGGTGTCTTTTAAATTTTGGCTTTTATGACTATCCAGCTCTGAGAG 275
DB 483 TGAGCTTTTGGTGTCTTTTAAATTTTGGCTTTTATGACTATCCAGCTCTGAGAG 542

QY 276 ACGGAGTTGAGTTGGCCCTTACCTTGGTGGGTGGGGGGGGCGGGCTGTT 335
DB 543 ACGGAGTTGAGTTGGCCCTTACCTTGGTGGGTGGGGGGGGCGGGCTGTT 602

QY 336 TGTTCCTTTTCTTTTAAAGTTGGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 215
DB 603 TGTTCCTTTTCTTTTAAAGTTGGGTTCACCTTGGAGTTTAAAGTTTCTTTGC 482

QY 396 TTCTCTCCCCACACCCCAAGTATTTGCACAAATTTTGTGCGGGGTATGGGGTGGT 455
DB 663 TTCTCTCCCCACACCCCAAGTATTTGCACAAATTTTGTGCGGGGTATGGGGTGGT 722

QY 456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCTCATTTTGGGGGTGTG 515
DB 723 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCTCATTTTGGGGGTGTG 782

Db TCTGAGTGAAGGGGCTGTCTGCCATCCACAAATGTGAGAGGGCGCCCGGTGTGGG 422
Qy 156 GTCCAGCTCTGACACTGCTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTGC 215
Db 423 GTCCAGCTCTGACACTGCTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTGC 482
Qy 216 TGAGCTTTTGGTGTGCTTTTATTTTGGCTTCTTATGACTATCCAGCTCTGAGAG 275
Db 483 TGAGCTTTTGGTGTGCTTTTATTTTGGCTTCTTATGACTATCCAGCTCTGAGAG 542
Qy 276 ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTGGGTTGGGGGGGGGGGGCTGTTT 335
Db 543 ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTGGGTTGGGGGGGGGGGGCTGTTT 602
Qy 336 TGTTCCTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCAACAGTGGGCGAGC 395
Db 603 TGTTCCTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCAACAGTGGGCGAGC 662
Qy 396 TTCTCCCCACACCAAGTATTTGCACAAATTTTGGCGGGTATGGGGTGGGTTT 455
Db 663 TTCTCCCCACACCAAGTATTTGCACAAATTTTGGCGGGTATGGGGTGGGTTT 722
Qy 456 AAATCTCGTTTCTTTGACAAAGCACAGGATCTCGTTCTCTCTATTTTGGGGTGTG 515
Db 723 AAATCTCGTTTCTTTGACAAAGCACAGGATCTCGTTCTCTCTATTTTGGGGTGTG 782
Qy 516 TGGGGACTTCTCAGTGTGTCGCCCGCTTCTGCAATCTTCTGCGCTTCTGCGGCGC 575
Db 783 TGGGGAC-TCTCAGTGTGTCGCCCGCTTCTGCAATCTTCTGCGCTTCTGCGGCGC 840
Qy 576 CGTCGGGAGGGCCCATG 592
Db 841 CGTCGGGAGGGCCCATG 857

RESULT 7
AL550979 954 bp mRNA linear EST 25-MAR-2004
LOCUS
DEFINITION AL550979 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS001065YD20 5-PRIME, mRNA sequence.
ACCESSION AL550979
VERSION AL550979.3 GI:45751340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Li, M.B., Gruber, C., Jessee, J. and Polayes, D.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 954)
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272796.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

Location/Qualifiers
1. .954
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001065YD20"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone libs="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was

FEATURES
source

digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 89.1%; Score 527.6; DB 1; Length 954;
Best Local Similarity 98.4%; Pred. No. 2.4e-123;
Matches 549; Conservative 4; Mismatches 3; Indels 2; Gaps 2;
Qy 36 CTGGAGTTGGTTCAGTTCAAGTTCTTCTCTGGCCCTTGGGGGCTTGGGGCCACC 95
Db 301 CTGGAGTTGGTTCAGTTCAAGTTCTTCTCTGGCCCTTGGGGGCTTGGGGCCACC 360
Qy 96 TCTGAGTGAAGGGGCTGTCTGCCCCATCCCAATGTGGAGAGGGCGCCCGGTGTGG 155
Db 361 TCTGAGTGAAGGGGCTGTCTGCCCCATCCCAATGTGGAGAGGGCGCCCGGTGTGG 420
Qy 156 GTCCAGCTCTGACACTGCTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTGC 215
Db 421 GTCCAGCTCTGACACTGCTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTGC 480
Qy 216 TGAGCTTTTGGTGTGTTCTTTTATTTTGGCTTCTTATGACTATCCAGCTCTGAGAG 275
Db 481 TGAGCTTTTGGTGTGTTCTTTTATTTTGGCTTCTTATGACTATCCAGCTCTGAGAG 540
Qy 276 ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTGGGTTGGGGGGGGGGCTGTTT 335
Db 541 ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTGGGTTGGGGGGGGGGCTGTTT 600
Qy 336 TGTTCCTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCAACAGT-GGGCGAG 394
Db 601 TGTTCCTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCAACAGTGGGGCGAG 660
Qy 395 CTTCCTCCCCACACCAAGTATTTGCACAAATTTTGTGGGGGTATGGGGGTGGGTTT 454
Db 661 CTTCCTCCCCACACCAAGTATTTGCACAAATTTTGTGGGGGTATGGGGGTGGGTTT 720
Qy 455 TAAATCTCGTTTCTTTGACAAAGCACAGGATCTCGTTCTCTCTCATTTTGGGGGTGT 514
Db 721 TAAATCTCGTTTCTTTGACAAAGCACAGGATCTCGTTCTCTCTCATTTTGGGGGTGT 780
Qy 515 GTGGGAGCTTCTCAGTGTGTCGCCCGCTTCTCTCAGTCCCTTCTGCCCTGCCGGGC 574
Db 781 GTGGGAGCTTCTCAGTGTGTCGCCCGCTTCTCTCAGTCCCTTCTGCCCTGCCGGGC 839
Qy 575 CGTCGGGAGGGCCCATG 592
Db 840 CGTCGGGAGGGCCCATG 857

RESULT 8
BI767860 868 bp mRNA linear EST 25-SEP-2001
LOCUS 603060979F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210323 5',
DEFINITION mRNA sequence.
ACCESSION BI767860
VERSION BI767860.1 GI:15759438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 868)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1527 row: n column: 20
High quality sequence stop: 848.
Location/Qualifiers

FEATURES

source
1. 868
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5210323"
/lab host="DH10B"
/clone lib="NIH MGC 122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 85.1%; Score 503.6; DB 3; Length 868;
Best Local Similarity 97.8%; Pred. No. 3.1e-117;
Matches 542; Conservative 0; Mismatches 9; Indels 3; Gaps 3;
QY 36 CTGGAGTTGGTTCAGTTCAAGTTTCCTTCCTGCGCCCTTGGGGGCTTGGGGCCACC 95
DB 316 CTGGAGTTGGTTCAGTTCAAGTTTCCTTCCTGCGCCCTTGGGGGCTTGGGGCCACC 375
QY 96 TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGGCCCGGCTGTGG 155
DB 376 TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGGCCCGGCTGTGG 435
QY 156 GTCCAGCTCTGGACACTGCTTGGGGCGGGTTCACCTTTCAGTTTAACTTCTTTTC 215
DB 436 GTCCAGCTCTGGACACTGCTTGGGGCGGGTTCACCTTTCAGTTTAACTTCTTTTC 495
QY 216 TGAGCTTTTGTGGTGTCTTTTATTTTGTGCTCTTTATGACTATCCAGCTCTGAGAG 275
DB 496 TGAGCTTTTGTGGTGTCTTTTATTTTGTGCTCTTTATGACTATCCAGCTCTGAGAG 555
QY 276 ACGGAGTTTGGAGTTGCGCGCTTACTTGGTGTGGTGGGGGGCGCGGGCTGTGT 335
DB 556 ACGGAGTTTGGAGTTGCGCGCTTACTTGGTGTGGTGGGGGGCGCGGGCTGTGT 615
QY 336 TGTTCCTTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCCAAACAGTGGCGAGC 395
DB 616 TGTTCCTTTTCTTTTAAAGTTGGGTTTCTTTTAAATATCCAAACAGTGGCGAGC 675
QY 396 TTCTCTCCCCACACCCCAAGTATTTGACAAATATTTGTGGGGGTATGGGGGT-GGGTTTT 454
DB 676 TTCTCTCCCCACACCCCAAGTATTTGACAAATATTTGTGGGGGTATGGGGGTCTCT 735
QY 455 TAAATCTGTTTCTCTTGGACAAGACAGGAGTCTGTTCTCTCTCATTTTTCGGGGTGT 514
DB 736 CAAATCTGTTTCTCTTGGACAAGACAGGAGTCTGTTCTCTCTCA-TTTAAGGGGGTGT 794
QY 515 GTGGGAGCTTCTCAGGTCGTGTCGCCAGCTTCTCTCAGTTCCTTCTGCGCTGCCGGGC 574
DB 795 GTGGGAGCTTCTCAGGTCGTGTCGCCAGGCTTCTCTCAGTTCCTTCTGCGCTGCCGGG- 853
QY 575 CCCTCGGGAGGCGC 588
DB 854 CCCTCGGGAGGCGC 867

RESULT 9
CX759082 706 bp mRNA linear EST 24-JAN-2005
LOCUS AGENCOURT_41357736 NIH_MGC_279 Homo sapiens cDNA clone
DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

IMAGE:7775009 3', mRNA sequence.
CX759082
CX759082.1 GI:58055738
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhardt, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcgpb3-r@mail.nih.gov
Tissue procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1521 row: 1 column: 15
High quality sequence stop: 677.
Location/Qualifiers

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7775009"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab host="DH10B Tona"
/clone lib="NIH MGC 279"
/notes="Organ: Blastocyst; Vector: pExpress-1; Site 1:
EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSP-1.14, NIH Registry designation UC01. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence. Passage 35. This line is a
subclone of the parental line; the parental line was
subcloned to remove aneuploid cells). cDNA was primed
using oligo-dT primer:
5'-pGACTAGTCTAGATCGAGCGCGCCCTT25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 1.82 kb. This
primary library is normalized (non-normalized primary
library is NIH_MGC_278) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Query Match 84.8%; Score 502; DB 8; Length 706;
Best Local Similarity 100.0%; Pred. No. 7.5e-117;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 CCACCTCTCAGTCAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCGGT 150
DB 1 CCACCTCTCAGTCAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCGGT 60
QY 151 GTGGGGTCCAGTCTGTGACACTGTCTGGCGGGGGTTCATTGAGTTTAAAGTTTTC 210
DB 61 GTGGGGTCCAGTCTGTGACACTGTCTGGCGGGGGTTCATTGAGTTTAAAGTTTTC 120
QY 211 TTGTGCTGAGCTTTTGGTGTCTTTTATTTTGGCTCTTTATGACTATCCAGTCT 270
DB 121 TTGTGCTGAGCTTTTGGTGTCTTTTATTTTGGCTCTTTATGACTATCCAGTCT 180
QY 271 GAGAGACGGGAGTTTGGAGTTGCGCGCTTACTTTTGGTGGGTGGGGGGCGCGGGC 330

Db 181 GAGACAGCGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTGGGGGGGGCGGCGGC 240
Qy 331 TGTCTTTGTTCTTTCTTTTAAAGATGGGTTTCTTTTAAATATCCAAACAGTGG 390
Db 241 TGTCTTTGTTCTTTCTTTTAAAGATGGGTTTCTTTTAAATATCCAAACAGTGG 300
Qy 391 GCAGCTTCTCTCCCAACACCCCAAGTATTTGCACAAATATTTGGCGGGGTATGGGGTGGG 450
Db 301 GCAGCTTCTCTCCCAACACCCCAAGTATTTGCACAAATATTTGGCGGGGTATGGGGTGGG 360
Qy 451 TTTTAAATCTCGTTCTCTTGGACACAGGACATCTCGTTCTCTCTCAATTTTGGGG 510
Db 361 TTTTAAATCTCGTTCTCTTGGACACAGGACATCTCGTTCTCTCTCAATTTTGGGG 420
Qy 511 GTGTGTGGGGACTTCTCAGGTGCTGTCGCCAGCTTCTCTCAGTCCCTTCTGCGCTGCC 570
Db 421 GTGTGTGGGGACTTCTCAGGTGCTGTCGCCAGCTTCTCTCAGTCCCTTCTGCGCTGCC 480
Qy 571 GGGCCCGTCGGAGGCGGCATG 592
Db 481 GGGCCCGTCGGAGGCGGCATG 502

RESULT 10
AL554544 947 bp mRNA linear EST 30-MAR-2004
LOCUS
DEFINITION
AL554544 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone: CS0D1083YD16 5-PRIME, mRNA sequence.

ACCESSION
AL554544
VERSION
AL554544.3 GI:45859296

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 947)

Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization

On Feb 15, 2001 this sequence version replaced gi:31276354.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1. 947

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1083YD16"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 83.8%; Score 495.8; DB 1; Length 947;

Best Local Similarity 93.2%; Pred. No. 3e-115;

Matches 521; Conservative 24; Mismatches 11; Indels 3; Gaps 3;

Qy 36 CTGAGTTGTTCAAGTTCAATTTCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 95

Db 303 CTGAGTTGTTCAAGTTCAATTTCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 362

Qy 96 TCTGAGTGAAGGGGCTGTCTGCCATCCACAATGTGGAGAGGGCGCCCGGTGTGGG 155
Db 363 TCTGAGTGAAGGGGCTGTCTGCCATCCACAATGTGGAGAGGGCGCCCGGTGTGGG 422
Qy 156 GTCCAGCTCTGGACACATGCTTTGGCGGGCGGTTTCACTTTGAGTTTAAAGTTCTTTTC 215
Db 423 GTCCARMTMTGGACAMTGTCTTGGCGGGCTTCACTTTGAATAATTAATAMMTTGC 482
Qy 216 TGAGCTTTTGGTGTGTCTTTTAAATTTTGGCTCTTTATGAC-TATCCAGCTCTGAGA 274
Db 483 TGAGCTTTTGGTGTGTCTTTTAAATTTTGGCTCTTTATGAC-TATCCAGCTCTGAGA 542
Qy 275 GACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGTGGGGGGGGCGGGCTGTT 334
Db 543 GAAAGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGTGGGGGGGGCGGGCTGTT 602
Qy 335 TTGTTCTCTTTCTTTTAAAGATGGTGTCTTTTAAATTTTAAATTTTAAATTTTAAATTTT 394
Db 603 TTGTTCTCTTTCTTTTAAAGATGGTGTCTTTTAAATTTTAAATTTTAAATTTTAAATTTT 662
Qy 395 CTTCCTCCCGCACACCCCAAGTATTTGCACATATTTGGCGGGGTATGGGGTGGGTTT 454
Db 663 CTTCCTCCCGCACACCCCAAGTATTTGCACATATTTGGCGGGGTATGGGGTGGGTTT 721
Qy 455 TAAATCTCGTTCTTCTGGACACAGCAGGATCTCGTTCTCTCTCATTTT-TGGGGTG 513
Db 722 TAAATCTCGTTCTTCTGGACACAGCAGGATCTCGTTCTCTCTCATTTT-TGGGGTG 781
Qy 514 TGTGGGAGCTTCTCAGTCTGTGTCTCCCGAGCTTCTCTGAGTCCCTTCTGCGCTGCCGG 573
Db 782 TGTGGGAGCTTCTCAGTCTGTGTCTCCCGAGCTTCTCTGAGTCCCTTCTGCGCTGCCGG 841
Qy 574 CCGTCTGGGAGGCGCCATG 592
Db 842 CCGTCTGGGAGGCGCCATG 860

RESULT 11

BI771877

LOCUS

DEFINITION

60305278F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204875 5',

mRNA sequence.

BI771877

ACCESSION

BI771877.1 GI:15763455

VERSION

EST.

KEYWORDS

Source

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 932)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLMI1513 row: k column: 20

High quality sequence stop: 887.

Location/Qualifiers

1. 932

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5204875"

/lab_host="DH10B"

/clone_lib="NIH_MGC_122"

/notes="Organ: pooled lung and spleen; Vector: PCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match	81.8%;	Score 484.2;	DB 3;	Length 932;
Best Local Similarity	97.6%;	Pred. No. 2.7e-112;		
Matches 534;	Conservative 0;	Mismatches 8;	Indels 5;	Gaps 4;

QY	36	CTGGAGTTGGTTCAGTTCAAGTTCAATCTTCCTCTGCGCCCTTGGGGGCTTGGGGCCACC	95
DB	312	CTGGAGTTGGTTCAGTTCAAGTTCAATCTTCCTCTGCGCCCTTGGGGGCTTGGGGCCACC	371
QY	96	TCTGAGTGAAGGGGCTGCTGCCCATCCACCAATGTGGAGAGCGCCCGCGTGTGGG	155
DB	372	TCTGAGTGAAGGGGCTGCTGCCCATCCACCAATGTGGAGAGCGCCCGCGTGTGGG	431
QY	156	GTCCAGC-TCTGGACACTGCTTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTG	214
DB	432	GTCCAGCTTCTGGACACTGCTTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTG	491
QY	215	CTGAGCTTTTGGTGTCTTTTAAAGTTTGGTTCCTTTTAAATTAATTCACATTCAGCTCTGAGA	274
DB	492	CTGAGCTTTTGGTGTCTTTTAAATTAATTTTGGCTCTTTTATGACTATCAGCTCTGAGA	551
QY	275	GACGGAGTTGAGTTGCGCGCTTACTTTGTTGGTGGGGGGCGCGGGCTGTT	334
DB	552	GACGGAGTTGAGTTGCGCGCTTACTTTGTTGGTGGGGGGCGCGGGCTGTT	611
QY	335	TGTTCTCTTTCTTTTAAAGTTGGTGTCTTTTAAATTAATTCACAACTGGGCGAG	394
DB	612	TGTTCTCTTTCTTTTAAAGTTGGTGTCTTTTAAATTAATTCACAACTGGGCGAG	671
QY	395	CTTCTCTCCCAACACCAAGTATTGACAATATTGTGGGGGTATGGGGTGGT	454
DB	672	CTTCTCTCCCAACACCAAGTATTGACAATATTGTGGGGGTATGGGGTGGG-TTC	729
QY	455	TAAATCTGTTCTCTTGGACAGCAGAGGATCTGCTCTCTCAATTTTTCGGGGTGT	514
DB	730	TAAATCTGTTCTCTTGGACAGCAGAGGATCTGCTCTCTCA--TTTTCGGGGTGT	787
QY	515	GTGGGACTTCTCAGGTCGTGTCGCCAGCTTCTCTGAGTCCCTTCTGCGCCCGCGGC	574
DB	788	GTGGGACTTCTCAGGTCGTGTCGCCAGCTTCTCTGAGTCCCTTCTGCGCTTCCCGGC	847
QY	575	CCGTGCG 581	
DB	848	CCGTGCG 854	

RESULT 12

LOCUS	BUI45820
DEFINITION	AGENCOURT 8137087 Lupsaki dorsal root ganglion Homo sapiens CDNA
CLONE IMAGE	6184135 5', mRNA sequence.
ACCESSION	BUI45820
VERSION	BUI45820.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE	Hominidae; Homo.
	1 (bases 1 to 966)
	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13572 row: n column: 08
High quality sequence stop: 568.

FEATURES

Location/Qualifiers	1..966
Source	1..966
Organization	"Homo sapiens"
Mol type	"mRNA"
db_xref	"taxon:9606"
clone	"IMAGE:6184135"
sex	"male"
tissue	"dorsal root ganglia"
dev stage	"adult, 36 yr"
lab host	"DH10B"
clone lib	"Lupski dorsal root ganglion"
note	"Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; CDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGAGCGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Query Match	80.2%;	Score 474.8;	DB 5;	Length 966;
Best Local Similarity	97.4%;	Pred. No. 6.7e-110;		
Matches 493;	Conservative 0;	Mismatches 12;	Indels 1;	Gaps 1;

QY	36	CTGGAGTTGGTTCAGTTCAAGTTCAATCTTCCTCTGCGCCCTTGGGGGCTTGGGGCCACC	95
DB	150	CTGGAGTTGGTTCAGTTCAAGTTCAATCTTCCTCTGCGCCCTTGGGGGCTTGGGGCCACC	209
QY	96	TCTGAGTGAAGGGGCTGTGCCCATCCAAATGTGGAGAGGGCGCCCGCGTGTGGG	155
DB	210	TCTGAGTGAAGGGGCTGTGCCCATCCAAATGTGGAGAGGGCGCCCGCGTGTGGG	269
QY	156	GTCCAGCTCTGACACTGCTTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTTC	215
DB	270	GTCCAGCTCTGACACTGCTTGGCGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTTC	329
QY	216	TCGAGCTTTTGGTGTCTTTTAAATTAATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG	275
DB	330	TCGAGCTTTTGGTGTCTTTTAAATTAATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG	389
QY	276	ACGGGAGTTGGAGTTGCGCGCTTTACTTTGGTGGGGGGCGCGCGGCTGTTT	335
DB	390	ACGGGAGTTGGAGTTGCGCGCTTTACTTTGGTGGGGGGCGCGCGGCTGTTT	449
QY	336	TGTTCTCTTTTCTTTTAAAGTTGGTGTCTTTTAAATTAATTCACAACTGGGCGAGC	395
DB	450	TGTTCTCTTTTCTTTTAAAGTTGGTGTCTTTTAAATTAATTCACAACTGGGCGAGC	509
QY	396	TTCTCTCCCCCACACCAAGTATTGACAAATTTGTGCGGGGTAT-GGGGGTGGGTTT	454
DB	510	TTCTCTCCCCCACACCAAGTATTGACAAATTTGTGCGGGGTATGGGGGTGGGTTT	569
QY	455	TAAATCTCGTTTCTCTTGGACAAGCAGGATCTCGTTCTCTCAATTTTTCGGGGTGT	514
DB	570	TAAATCTCGTTTCTCTTGGACAAGCAGGATCTCGTTCTCTCAATTTTTCGGGGCGC	629
QY	515	GTGGGACTTCTCAGTCTGTGTCGCC	540

```

Db      630 GTGGAGACCTCTCCGTCAGAACCC 655

RESULT 13
AL549255
LOCUS
DEFINITION
AL549255 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1049YH08 5-PRIME, mRNA sequence.
ACCESSION
AL549255
VERSION
AL549255.3 GI:45749657
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 904)
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:31271075.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1049YH08"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 76.6%; Score 453.6; DB 1; Length 904;
Best Local Similarity 88.4%; Pred. No. 1.7e-104;
Matches 495; Conservative 23; Mismatches 39; Indels 3; Gaps 3;
QY      36 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGGCTTGGGGCCACC 95
Db      315 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGGCTTGGGGCCACC 374
QY      96 TCTGAGTGAAGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGCGCCCGCGTGTGG 155
Db      375 TCTGAGTGAAGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGCGCCCGCGTGTGG 434
QY      156 GTCCAGTCTGGACACGCTTGGCGGGGCTTCACTTGAAGTTTAAAGTTCTTTTGC 215
Db      435 GTCCAGTCTGGACACGCTTGGCGGGGCTTCACTTGAAGTTTAAAGTTCTTTTGC 494
QY      216 TGAGCTTTTGGTGTCTTTTATTTTGGCTTTATGATCTACATCCAGCTCTGAGAG 275
Db      495 TGAGCTTTTGGTGTCTTTTATTTTGGCTTTATGATCTACATCCAGCTCTGAGAG 554
QY      276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGTGGGGGGCGGGCGGCTGTTT 335
Db      555 AAGGGCGTTGGGGTTCACCCACTTAAATTTGGTTGGTGGGGGGGSGSGCTGTTT 614
QY      336 TGTTCCTTTTAAAGTTGGGTTTCTTTTAAATTTAAATTTAAATTTAAATTTAAATTT 393
Db      615 TGTTCCTTTTAAAGTTGGGTTTCTTTTAAATTTAAATTTAAATTTAAATTTAAATTT 674
QY      394 GCTTCTCTCCCCACACCCAGATTATTCACAAATATTTGTGGGGGTATGGGGGTGGGTTT 453

Db      675 RCTTCTCTCCCCACACCCAAATATTTGCAAAATATTTGTGGGGGTATGGGGGTGGGTTT 734
QY      454 TTAATCTCGTTTCTTCTTGGACACAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 512
Db      735 TTAATCTCGTTTCTTCTTGGACACAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 794
QY      513 GTGGGGGACTTCTCAGTGTGTGCCCCAGCCTTCTCTGAGTCCCTTCTGCCCCCTGCCGG 572
Db      795 GTGGGGGACTTCTCAGTGTGTGCCCCAGCCTTCTCTGAGTCTCTCTGAGTCTCTCTGCC 854
QY      573 GCCCGTCGGGAGCGCCCATG 592
Db      855 GCCCGTCGGGAGCGCCCATG 874

RESULT 14
BI770311 940 bp mRNA linear EST 25-SEP-2001
LOCUS
DEFINITION
603056215F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205698 5',
mRNA sequence.
ACCESSION
BI770311 GI:15761889
VERSION
BI770311
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 940)
AUTHORS
NTH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@xmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1515 row: n column: 03
High quality sequence stop: 862.
FEATURES
Location/Qualifiers
1..940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5205698"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 76.6%; Score 453.4; DB 3; Length 940;
Best Local Similarity 94.3%; Pred. No. 1.9e-104;
Matches 525; Conservative 0; Mismatches 26; Indels 6; Gaps 5;
QY      36 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGGCTTGGGGCCACC 95
Db      327 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGGCTTGGGGCCACC 386
QY      96 TCTGAGTGAAGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGCGCCCGCGTGTGG 155

```

387	Db	TCTGAGTGAAGGGGCTGTCTGCCCATCCAAATGTGGAGAGGGCGCCCCGGTGTGGG	446
156	Qy	GTCAGAGCTCTGGACACTGCTTGGCGCGCGGGTTCACTTTGAGTATTTAAAGTATTTCTTTGC	215
447	Db	GTCAGAGCTCTGGACACTGCTTGGCGCGCGGGTTCACTTTGAGTATTTAAAGTATTTCTTTGC	506
216	Qy	TGAGCTTTTGGTGTGTTCTTTTATTTTGGCTCTTTATGACTATCAGACTCTGAGAG	275
507	Db	TGAGCTTTTGGTGTGTTCTTTTATTTTGGCTCTTTATGACTATCAGACTCTGAGAG	566
276	Qy	ACGGAGTTTGGAGTTGCCCGCTTTTACTTTGGTTGGGGGGCGCGGGCGTGT	335
567	Db	ACGGAGTTTGGAGTTGCCCGCTTTTACTTTGGTTGGGGGGCGCGGGCGTGT	626
336	Qy	TGTTCTTTTCTTTTAAAGAGTTGGTGTTCCTTTTAAATATCCAAACAGTGGGCAGC	395
627	Db	TGTTCTTTTCTTTTAAAGAGTTGGG-TTTCCTTTTAAATATCCAAACAGTGGGCAGC	685
396	Qy	TTCTTCCCCACACCCAAAGTATTTGCACAAATATTTGTGCGGGGTATGGGGGTGGTTTT	455
686	Db	TTCTTCCCCACA-ACCCAAAGTATTTGCACAAATATTTGTGCGGGGTATGGCGCGTGGGGT	744
456	Qy	AAATCTCGTTTCTCTTGGACAGCACAGGATCTCGTTCTCTCTCAATTTTTCGGGGGTG	515
745	Db	AAATCTCGTTTCTCTTGGACAGGCACA-GGATCTCGTTCTCTCTCA-TTTAAGGGGGGTG	802
516	Qy	TGGGGACTTCTCAGTCCGTGTCCCCAGCCCTTCTCTGCAGTCCCTTCTGCCCCGCCGGGC	575
803	Db	TGGGGACTTCTCAGTCCGTGTCCCCAGGCTTATCTGAAGTCC--TTCTGCCCTCGCGGGCC	860
576	Qy	CGTCGGAGGCGCCCATG	592
861	Db	CGTCGGAGGCGCCCATG	877

RESULT 15
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 LOCUS
 DEFINITION
 BI834269 861 bp mRNA linear EST 04-OCT-2001
 60308417BP1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223331 5',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNML1561 Row: 1 column: 20
 High quality sequence stop: 830.
 Location/Qualifiers
 1. 861
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5223331"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector:

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:30 ; Search time 467 Seconds
(without alignments)
8448.604 Million cell updates/sec

Title: US-10-624-670-1

Perfect score: 592

Sequence: 1 ctatagggaacgctgtgtcg.....gccctcgaggagcccatg 592

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq 21:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	592	12	ADJ57079 Metastati
2	557	94.1	1692	10	ADQ99124 Human KPP
3	557	94.1	2181	12	ADQ22123 Human sof
4	557	94.1	2850	6	ABL92112 Human Tum
5	557	94.1	2850	10	ABX72037 DNA encod
6	555	93.8	909	12	ADJ28112 Human PRL
7	551	93.1	986	12	ADJ57080 Metastati
8	410.6	69.4	1859	10	ADQ99125 Human KPP
9	337	56.9	1320	11	ADN95384 Human BEC
10	337	56.9	1321	12	ADJ28097 Human pro
11	337	56.9	1321	12	ADJ57209 Human PRL
12	337	56.9	1321	12	ADP21390 Gene PTP4
13	337	56.9	1396	12	ADJ28111 Human pro
14	337	56.9	1396	12	ADN75973 Human sig
15	337	56.9	1396	12	ADP28082 Human pro
16	334	56.4	334	13	ADL12326 Human pro
17	310	52.4	982	10	ACA56395 Human sig
18	310	52.4	982	12	ADJ56191 Human pol
19	310	52.4	984	2	AAV29127 HPTP-2 CO

20	274.4	46.4	671	12	ADI28113	Human PRL
21	240	40.5	462	12	ADQ17386	Human sof
22	240	40.5	1006	12	ADI28332	Human pro
23	240	40.5	1006	14	AEA36203	Human nuc
24	236.4	39.9	358	3	AAA43595	Human sec
25	234	39.5	1315	3	AAA09025	Human CSA
26	221	37.3	773	12	ADO26263	C35 promo
27	139	23.5	1678	12	ADI28192	Mouse CDN
28	131.4	22.2	3222	12	ADI28104	Human col
29	64	10.8	527	14	ACL56361	Human col
30	58	9.8	396	13	ACN63020	Cotton ca
31	52.8	8.9	363	13	ACN45489	Cotton pr
32	52.8	8.9	1260	6	ABQ16903	Oligonuel
33	52.8	8.9	1260	6	ABQ16902	Oligonuel
34	52	8.8	7758	6	ABL33103	Human imm
35	51.2	8.6	192	13	ACN50408	Cotton ma
36	51	8.6	629	10	ABT21705	Breast ca
37	50.8	8.6	7698	6	ABL33700	Human imm
38	50.4	8.5	1025	6	ABQ25831	Oligonuel
39	50.4	8.5	1025	6	ABQ25830	Oligonuel
40	49.2	8.3	509	6	ABQ18800	Oligonuel
41	49.2	8.3	509	6	ABQ18801	Oligonuel
42	48.8	8.2	7721	14	AEA18095	Converted
43	48.6	8.2	565	6	ABQ17072	Oligonuel
44	48.6	8.2	565	6	ABQ17073	Oligonuel
45	48.6	8.2	5203	10	ADB54278	Precreate

ALIGNMENTS

RESULT 1

ADJ57079
ID ADJ57079 standard; DNA; 592 BP.

AC ADJ57079;

XX 06-MAY-2004 (first entry)

XX Metastatic colon cancer-specific transcriptional regulatory element.

XX Human; PRL-3; promoter; transcriptional regulatory element; gene therapy; colon cancer; metastasis; cytostatic; gene therapy; ds.

XX Homo sapiens.

XX WO2004009790-A2.

XX 29-JAN-2004.

XX 22-JUL-2003; 2003WO-US023032.

XX 22-JUL-2002; 2002US-0397859P.

XX (CELL-) CELL GENESYS INC.

XX Li Y, Yu DC;

XX WPI; 2004-123388/12.

XX New colon cancer transcriptional regulatory element (TRE) sequence that is specific for metastatic colon cancer cells, useful as a promoter for specific virus replication.

XX Claim 4; SEQ ID NO 1; 39pp; English.

XX The present sequence is that of a colon cancer transcriptional regulatory element (TRE) derived from the human PRL-3 gene in the region upstream of the translational start codon. The PRL-3 protein tyrosine phosphatase gene is specifically expressed at a high level in metastatic colon cancers. The invention provides replication-competent adenoviral vectors comprising the present sequence operably linked to a gene required for virus replication. Methods are provided for introducing into a cell an

Qy	216	TGAGCTCTTTTGGTGTCTCTTTTAAATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG	275
Db	660	TGAGCTCTTTTGGTGTCTCTTTTAAATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG	719
Qy	276	ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGGGGGGCGGGGGCTGTGTT	335
Db	720	ACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGGGGGGCGGGGGCTGTGTT	779
Qy	336	TGTTCTCTTTCTTTTAAAGAGTTGGGTTTCTTTTAAATATCCAAACAGTGGGCAGC	395
Db	780	TGTTCTCTTTCTTTTAAAGAGTTGGGTTTCTTTTAAATATCCAAACAGTGGGCAGC	839
Qy	396	TTCTCTCCCCACACCCAAAGTATTTGCACAAATATTTGTGCGGGGTATGGGGTGTGGT	455
Db	840	TTCTCTCCCCACACCCAAAGTATTTGCACAAATATTTGTGCGGGGTATGGGGTGTGGT	899
Qy	456	AAATCTCGTTTCTCTTGGACAAGCACAGGGAATCTCGTTCTCCTCATTTTMTTGGGGGTGTG	515
Db	900	AAATCTCGTTTCTCTTGGACAAGCACAGGGAATCTCGTTCTCCTCATTTTMTTGGGGGTGTG	959
Qy	516	TGGGGACATTCTCAGTCTGTGTCCCAGCGTTCTCTGACAGTCCCTTCTGSCCCTGCCGGGCC	575
Db	960	TGGGGACATTCTCAGTCTGTGTCCCAGCGTTCTCTGACAGTCCCTTCTGSCCCTGCCGGGCC	1019
Qy	576	CGTCGGGAGGCCCATG	592
Db	1020	CGTCGGGAGGCCCATG	1036

RESULT 3

ADQ22123
ID ADQ22123 standard: DNA: 2181 BP.

XX
AC ADO22123:

XX
DT 26-AUG-2004 . (first entry)

XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4943.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; KW ds.

XX
OS Homo sapiens.

XX PN WO2004048938-A2.

XX
PD 10-JUN-2004.

XX
PF
26-NOV-2003; 2003WO-US038193.

XX
PR 26-NOV-2002; 2002US-0429739P;
XX

XX
PA (PROT-) PROTEIN DESIGN LABS. INC.

XX
PI Aziz N, Ginsburg WM, Zlotnik A;

XX
DR WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX
PS Example 2; SEQ ID NO 4943; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has

cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

XX
SQ Sequence 2181 BP; 512 A; 649 C; 546 G; 474 T; 0 U; 0 Other;

Query Match 94.1%; Score 557; DB 12; Length 2181;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 557; Conservative 0; Mismatches 0; Indels 0

QY 36 CTGGAGTTGGTTTCAGTTTCAAGTTTCATTCTTCCCTCTGGGCCCTTGGGGGCTTGGGGCCACC 95

Db 316 CTGGAGTTGGTTTCAGTTTCAAGTTTCATTCCTCTGGGCCCTTGGGGGGCTTGGGGCCACC 375

QY 96 TCTGACTGAAGGGGGCTGTCTGCGCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 155

Db 376 TCTGAGTGAAGGGGGTGTCTGCCCATCCACCAATGTGGAGAGGGGGCCCCCGGTGTGGG 435

Qy 156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGTTCACATTGAGCTTTTAAAGTTTCTTTGC 215

Db 436 GTCCAGCTCTGGACATGCTTGGGGCCGGGTTCATTGAGTTTTTAAGTTTTCTTTGC 495

QY 216 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG 275

Db 496 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGGCTTGAGAG 555

Qy 276 ACGGAGT^{TT}TGGAGT^{TT}TGCCCGCTTTAC^{TT}TGGT^{TT}TGGGT^{TT}TGGGGGGGGCGCGCGGCTGT^{TT}T 335

D**b** 556 ACGGGAGTTTGGAGTTGCCCG

RESULT 4

ABL92112
ID ABL92112 standard; cDNA; 2850 BP.

XX ABL92112;

XX
DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 247.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cystostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.

XX Homo sapiens.
OS

XX
PN
WO200210217-A2.

XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US024031.
XX PR 02-AUG-2000; 2000US-0222599P.
XX PR 11-AUG-2000; 2000US-0224360P.
XX PR 11-APR-2001; 2001US-0282850P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI St Croix B, Kinzler KW, Vogelstein B;
XX DR WPI; 2002-291856/33.
XX DR P-PSDB; ABB90758.
XX PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX PS Claim 65; Page 240; 331pp; English.
XX CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91986-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX SQ Sequence 2850 BP; 452 A; 863 C; 916 G; 619 T; 0 U; 0 Other;
Query Match 94.1%; Score 557; DB 6; Length 2850;
Best Local Similarity 100.0%; Pred. No. 3e-133;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 CTGGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 95
DB 345 CTGAGTTGGTTCAGTTCAAGTTCAATCTCTCTGCGCCCTTGGGGCTTGGGGCCACC 404
QY 96 TCTGAGTGAAGGGGCTGTCTGCCATCCCAATGTGGAGAGGGCCGCCCGTGTGG 155
DB 405 TCTGAGTGAAGGGGCTGTCTGCCATCCCAATGTGGAGAGGGCCGCCCGTGTGG 464
QY 156 GTCCAGCTCTGGACACTGCTTGGGGCGGGTTCACCTTTCAGTTTTCCTTTC 215
DB 465 GTCCAGCTCTGGACACTGCTTGGGGCGGGTTCACCTTTCAGTTTTCCTTTC 524
QY 216 TGAGCTTTTGGTGTCTTTTATTTTGGCTCTTATGACTATCCAGCTCTCAGAG 275
DB 525 TGAGCTTTTGGTGTCTTTTATTTTGGCTCTTATGACTATCCAGCTCTCAGAG 584
QY 276 ACGGAGTTTGGAGTTGCCCGCTTACTTTGGTGGGTGGGGGGCGCGCGCTGTTT 335
DB 585 ACGGAGTTTGGAGTTGCCCGCTTACTTTGGTGGGTGGGGGGCGCGCGCTGTTT 644
QY 336 TGTTCCTTTCTTTTAAAGAGTTGGTTTCTTTTATTAATCAACAGTGGGCAGC 395
DB 645 TGTTCCTTTCTTTTAAAGAGTTGGTTTCTTTTATTAATCAACAGTGGGCAGC 704
QY 396 TTCTCTCCACACACCAAGTATTTGGCAATATTTGTGGGGGTATGGGGTGGTTT 455
DB 705 TTCTCTCCACACACCAAGTATTTGGCAATATTTGTGGGGGTATGGGGTGGTTT 764
QY 456 AATATCTCGTTCTCTTGGACACAGCAGGAGTCTCGTTCTCTCTCATTTTTTGGGGGTGTG 515
DB 765 AATATCTCGTTCTCTTGGACACAGCAGGAGTCTCGTTCTCTCTCATTTTTTGGGGGTGTG 824

QY 516 TGGGGACTTCTCAGTCTGTGTCCCGAGCCTTCTCTGCACTCCCTTCTGCGCCGCCGCC 575
DB 825 TGGGGACTTCTCAGTCTGTGTCCCGAGCCTTCTCTGCACTCCCTTCTGCGCCGCCGCC 884
QY 576 CGTCGGAGGGGCCCATG 592
DB 885 CGTCGGAGGGGCCCATG 901
RESULT 5
ABX72037
ID ABX72037 standard; DNA; 2850 BP.
XX AC ABX72037;
XX DT 12-MAR-2003 (first entry)
XX DE DNA encoding human tumour endothelial marker TEM 29.
XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neoangiogenesis; immune response; cytostatic; antidiabetic; gene;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; da.
XX OS Homo sapiens.
XX PN WO200283874-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US008253.
XX PR 11-APR-2001; 2001US-0282850P.
XX PR 06-FEB-2002; 2002US-0354262P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX DR P-PSDB; ABUS4465.
XX PT New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX PS Disclosure; Page: 263-264; 374pp; English.
XX CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. The present
CC sequence represents a human TEM or NEM gene of the invention
XX SQ Sequence 2850 BP; 452 A; 863 C; 916 G; 619 T; 0 U; 0 Other;
Query Match 94.1%; Score 557; DB 10; Length 2850;
Best Local Similarity 100.0%; Pred. No. 3e-133;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 CTGGAGTTGGTTCAGTTCAAGTTCAATCTCTGCGCCCTTGGGGCTTGGGGCCACC 95

Db 345 CTGGAGTTGGTTCAAGTTCAATCTCTCTGGCCCTTGGGGCTTGGGGCCACC 404
QY 96 TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGAGAGGGGGCCCGGCTGGG 155
Db 405 TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGAGAGGGGGCCCGGCTGGG 464
QY 156 GTCCAGCTCTGGACATCTGTCTGGGGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTC 215
Db 465 GTCCAGCTCTGGACATCTGTCTGGGGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTC 524
QY 216 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG 275
Db 525 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG 584
QY 276 ACGGAGTTTGAAGTTGGCCGCTTACTTTGGTGGGTTGGGGGGCGGGCGGCTGTTT 335
Db 585 ACGGAGTTTGAAGTTGGCCGCTTACTTTGGTGGGTTGGGGGGCGGGCGGCTGTTT 644
QY 336 TGTTCCTTTCTTTTAAAGTTGGTCTTTCTTTTAAATATCAAAACAGTGGGCAGC 395
Db 645 TGTTCCTTTCTTTTAAAGTTGGTCTTTCTTTTAAATATCAAAACAGTGGGCAGC 704
QY 396 TTCTCTCCCCACACCAAGTATTTGACAAATATTTGCGGGGTATGGGGGTGGGTTTTT 455
Db 705 TTCTCTCCCCACACCAAGTATTTGACAAATATTTGCGGGGTATGGGGGTGGGTTTTT 764
QY 456 AAATCTCGTTTCTCTTGGACAAGCAGAGGATCTCGTCTCTCTCAATTTTGGGGGTGG 515
Db 765 AAATCTCGTTTCTCTTGGACAAGCAGAGGATCTCGTCTCTCTCAATTTTGGGGGTGG 824
QY 516 TGGGAGCTTCTCAGGTCTGTCTCCCAAGCTTCTCTGAGTCCCTTCTGCCCTGCCGGGCC 575
Db 825 TGGGAGCTTCTCAGGTCTGTCTCCCAAGCTTCTCTGAGTCCCTTCTGCCCTGCCGGGCC 884
QY 576 CGTCCGGAGGCCCATG 592
Db 885 CGTCCGGAGGCCCATG 901

RESULT 6

AD128112
ID AD128112 standard; cDNA; 909 BP.
AC AD128112;
DT 22-APR-2004 (first entry)
XX Human PRL3 cDNA #2 5' extension #1.
DE Human; antisense gene therapy; ss; PRL3;
KW protein tyrosine phosphatase type IVA member 3; colorectal cancer;
KW diabetes; glucose tolerance; insulin resistance; obesity;
KW hyperproliferative disorder; cytostatic.
XX Homo sapiens.
OS
XX
PN US2003235911-A1.
XX
PD 25-DEC-2003.
XX
PF 20-JUN-2002; 2002US-00177554.
XX
PR 20-JUN-2002; 2002US-00177554.
XX
XX (ISIS-) ISIS PHARM INC.
PA
PI Dobie KW, Zhang H;
XX
XX WPI; 2004-070585/07.
DR
XX
PT New antisense oligonucleotide, comprising a sequence targeted to a
PT nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
PT -3), useful for preparing a composition for treating hyperproliferative

disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 19; 77pp; English.
XX
CC The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
CC phosphatase type IVA member 3 (PRL-3), that specifically hybridizes with
CC the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
CC an antisense oligonucleotide (AO). Also included are a composition
CC comprising the compound and a carrier or diluent, inhibiting the
CC expression of PRL-3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with PRL-3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer (e.g. colorectal cancer), diabetes,
CC reduced glucose tolerance, insulin resistance and obesity. The present
CC sequence is a Human PRL3 target cDNA sequence.
XX
SQ Sequence 909 BP; 120 A; 273 C; 271 G; 242 T; 0 U; 3 Other;
Query Match 93.8%; Score 555; DB 12; Length 909;
Best Local Similarity 99.6%; Pred. No. 6.9e-133;
Matches 555; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 36 CTGAGATTGGTTCAAGTTCAAGTTCAATCTCTCTGGCCCTTGGGGCTTGGGGCCACC 95
Db 317 CTGAGATTGGTTCAAGTTCAAGTTCAATCTCTCTGGCCCTTGGGGCTTGGGGCCACC 376
QY 96 TCTGAGTGAAGGGGCTGTCTGCCCATCCACAAATGTGGAGAGGGCGGCCCGGTGTGG 155
Db 377 TCTGAGTGAAGGGGCTGTCTGCCCATCCACAAATGTGGAGAGGGCGGCCCGGTGTGG 436
QY 156 GTCCAGCTCTGGACATCTGTGGGGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTC 215
Db 437 GTCCAGCTCTGGACATCTGTGGGGCGGGTTCACCTTTGAGTTTAAAGTTTCTTTC 496
QY 216 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG 275
Db 497 TGAGCTTTTGGTGTCTCTTTTATTTTGGCTCTTTATGACTATCCAGCTCTGAGAG 556
QY 276 ACGGAGTTTGAAGTTGGCCGCTTCTTGGTGGGTTGGGGGGCGGGCGGCTGTTT 335
Db 557 ACGGAGTATGAGTTGGCCGCTTCTTGGTGGGTTGGGGGGCGGGCGGCTGTTT 616
QY 336 TGTTCCTTTCTTTTAAAGTTGGGTTCTTTTAAATATCAAAACAGTGGGCAGC 395
Db 617 TGTTCCTTTCTTTTAAAGTTGGGTTCTTTTAAATATCAAAACAGTGGGCAGC 676
QY 396 TTCTCTCCCCACACCAAGTATTTGACAAATATTTGCGGGGTATGGGGGTGGGTTTTT 455
Db 677 TTCTCTCCCCACACCAAGTATTTGACAAATATTTGCGGGGTATGGGGGTGGGTTTTT 736
QY 456 AAATCTCGTTTCTCTTGGACAAGCAGAGGATCTCGTCTCTCATTTTGGGGGTGTG 515
Db 737 AAATCTCGTTTCTCTTGGACAAGCAGAGGATCTCGTCTCTCATTTTGGGGGTGTG 796
QY 516 TGGGAGCTTCTCAGGTCTGTCTCCCAAGCTTCTCTGAGTCCCTTCTGCCCTGCCGGGCC 575
Db 797 TGGGAGCTTCTCAGGTCTGTCTCCCAAGCTTCTCTGAGTCCCTTCTGCCCTGCCGGGCC 856
QY 576 CGTCCGGAGGCCCATG 592
Db 857 CGTCCGGAGGCCCATG 873
RESULT 7
ADJ57080
ID ADJ57080 standard; DNA; 986 BP.
XX
XX AC ADJ57080;
XX
XX DT 06-MAY-2004 (first entry)
XX

DE Metastatic colon cancer-specific transcriptional regulatory element.
 XX Human; PRL-3; promoter; transcriptional regulatory element; gene therapy;
 KW colon cancer; metastasis; cytostatic; gene therapy; ds.
 OS Homo sapiens.
 XX WO2004009790-A2.
 PN 29-JAN-2004.
 PD 22-JUL-2003; 2003WO-US023032.
 XX 22-JUL-2002; 2002US-0397859P.
 XX (CELL-) CELL GENESYS INC.
 PA Li Y, Yu DC;
 PI WPI; 2004-123388/12.
 XX New colon cancer transcriptional regulatory element (TRE) sequence that
 PT is specific for metastatic colon cancer cells, useful as a promoter for
 PT specific virus replication.
 XX Claim 5; SEQ ID NO 2; 39pp; English.
 XX The present sequence is that of a colon cancer transcriptional regulatory
 CC element (TRE) derived from the human PRL-3 gene in the region upstream of
 CC the translational start codon. The PRL-3 protein tyrosine phosphatase
 CC gene is specifically expressed at a high level in metastatic colon
 CC cancers. The invention provides replication-competent adenoviral vectors
 CC comprising the present sequence operably linked to a gene required for
 CC virus replication. Methods are provided for introducing into a cell an
 CC adenoviral vector comprising a metastatic colon cancer-specific TRE
 CC operably linked to a gene required for virus replication, and host cells
 CC comprising the adenovirus vector. Methods are also provided for
 CC conferring selective cytotoxicity in target colon cancer cells,
 CC particularly metastatic colon cancer cells, by contacting the cells with
 CC an adenovirus vector of the invention, where the vector enters the cell
 CC and propagates virus. By providing for transcriptional initiating
 CC regulation dependent upon transcription factors that are only active in
 CC specific, limited cell types, virus replication is restricted to target
 CC cells.
 XX Sequence 986 BP; 131 A; 289 C; 289 G; 277 T; 0 U; 0 Other;
 SQ
 Query Match 93.1%; Score 551; DB 12; Length 986;
 Best Local Similarity 100.0%; Pred. No. 7.6e-132;
 Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 CTGGAGTTGGTTCAGTTCAAGTTCAATTCCTCTGGCCCTTGGGGCTTGGGGCCACC 95
 DB 436 CTGGAGTTGGTTCAGTTCAAGTTCAATTCCTCTGGCCCTTGGGGCTTGGGGCCACC 495
 QY 96 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCCCGCTGTGGG 155
 DB 496 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCCCGCTGTGGG 555
 QY 156 GTCCAGCTCTGGACACTGCTTGGCGGGGTTCACTTGAAGTTTAAAGTTCTTTTTC 215
 DB 556 GTCCAGCTCTGGACACTGCTTGGCGGGGTTCACTTGAAGTTTAAAGTTCTTTTTC 615
 QY 216 TGAGCTTTTGGTGTCTTTTATTTTGGCTCTTATGACTATCCAGCTCTGAGAG 275
 DB 616 TGAGCTTTTGGTGTCTTTTATTTTGGCTCTTATGACTATCCAGCTCTGAGAG 675
 QY 276 ACGGGAGTTGGAGTTCGCCCTTTACTTTGGTGGTGGGGGGCGGGGGCTGTTT 335
 DB 676 ACGGGAGTTGGAGTTCGCCCTTTACTTTGGTGGTGGGGGGCGGGGGCTGTTT 735
 QY 336 TGTTCCTTTTCTTTTAAAGAGTTGGGTTTCTTTTAAATATCCAAACAGTGGGCAGC 395

DB 736 TGTTCCTCTTTTCTTTTAAAGAGTGGGTTTCTTTTAAATATCCAAACAGTGGGCAGC 795
 QY 396 TTCTCTCCCCACACACCAAGTATTTGCAATATTTGCGGGGTATGGGGTGGGTTTTT 455
 DB 796 TTCTCTCCCCACACCAAGTATTTGCAATATTTGCGGGGTATGGGGTGGGTTTTT 855
 QY 456 AAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCTCTCTCATTTTGGGGGTGTG 515
 DB 856 AAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCTCTCTCATTTTGGGGGTGTG 915
 QY 516 TGGGGAGTTTCTCAGTCTGTCCTCCAGCCTTCTCTGCACTCCCTTGCCTGCCCGGCC 575
 DB 916 TGGGGAGTTTCTCAGTCTGTCCTCCAGCCTTCTCTGCACTCCCTTGCCTGCCCGGCC 975
 QY 576 CGTCGGGAGGC 586
 DB 976 CGTCGGGAGGC 986
 RESULT 8
 ADC99125
 ID ADC99125 standard; cDNA; 1859 BP.
 XX AC ADC99125;
 XX 01-JAN-2004 (first entry)
 XX Human KPP cDNA - SEQ ID 78.
 DE anti-HIV; anti-allergic; anti-inflammatory; antianemic; antiparkinsonian;
 XX neurotropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
 KW osteoplastic; antihypertensive; antiparasitic; antihelminthic; antipsoriatic;
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
 KW virucide; protozoicide; fungicide; kinase; phosphatase; KPP;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 KW cancer; developmental; mental retardation; neurological;
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 KW helminthic infection; transgenic; gene therapy; human; ss; gene.
 XX Homo sapiens.
 XX WO2003033680-A2.
 XX 24-APR-2003.
 XX 17-OCT-2002; 2002WO-US033723.
 XX 19-OCT-2001; 2001US-0345474P.
 PR 02-NOV-2001; 2001US-0343910P.
 PR 13-NOV-2001; 2001US-0333098P.
 PR 16-NOV-2001; 2001US-0332424P.
 PR 30-NOV-2001; 2001US-0334288P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Bandnan O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 PI Emerling BM, Forsythe IV, Gandhi AR, Gorvad AE, Griffin JA;
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang Y;
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 PI Zebbarjadian Y;
 XX WPI; 2003-403214/38.
 DR P-PSDB; ADC99073.
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.

Db 301 CCTTCTGCGTCCGGGCGCGTTCGGGAGGCCCATG 337

RESULT 10

ADI28097
ADI28097 standard; cDNA; 1321 BP.

AC ADI28097;

XX 22-APR-2004 (first entry)

XX Human protein tyrosine phosphatase, PRL3, variant 1 cDNA.

XX Human; antisense gene therapy; ss; PRL3;

XX protein tyrosine phosphatase type IVA member 3; colorectal cancer;

XX diabetes; glucose tolerance; insulin resistance; obesity;

XX hyperproliferative disorder; cytostatic.

XX Homo sapiens.

XX US2003235911-A1.

XX 25-DEC-2003.

XX 20-JUN-2002; 2002US-00177554.

XX 20-JUN-2002; 2002US-00177554.

XX (ISIS-) ISIS PHARM INC.

XX Dobie KW, Zhang H;

XX WPI; 2004-070585/07.

XX P-PSDB; ADI28333.

XX New antisense oligonucleotide, comprising a sequence targeted to a
XX nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
XX -3), useful for preparing a composition for treating hyperproliferative
XX disorders, e.g., cancer.

XX Example 13; SEQ ID NO 4; 77pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80
XX base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
XX phosphatase type IVA member 3 (PRL-3), that specifically hybridises with
XX the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
XX an antisense oligonucleotide (AO). Also included are a composition
XX comprising the compound and a carrier or diluent, inhibiting the
XX expression of PRL-3 in cells or tissues, treating an animal having or
XX suspected of having a disease or condition associated with PRL-3 and
XX screening for an antisense compound. The antisense oligonucleotide is
XX useful for preparing a composition for treating hyperproliferative
XX disorder, particularly cancer (e.g. colorectal cancer), diabetes,
XX reduced glucose tolerance, insulin resistance and obesity. The present
XX sequence is a Human PRL3 target cDNA sequence.

XX SQ Sequence 1321 BP; 267 A; 388 C; 376 G; 290 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGGAGTTGCCCTTACTTTGGTTGGTTG 315
Db 1 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGGAGTTGCCCTTACTTTGGTTGGTTG 60

QY 316 GGGGGGGGGCGGCTTTTGTCTCTTTTAAAGAGTGGGTTTCTTTTAA 375
Db 61 GGGGGGGGGCGGCTTTTGTCTCTTTTAAAGAGTGGGTTTCTTTTAA 120

QY 376 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAGATATTTGCCAATATTTGTGCG 435
Db 121 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAGATATTTGCCAATATTTGTGCG 180

QY 436 GGGTATGGGGTGGGTTTTTAATCTCGTTTCTTTGGACAAGCACAGGATCTCGTTCT 495
Db 181 GGGTATGGGGTGGGTTTTTAATCTCGTTTCTTTGGACAAGCACAGGATCTCGTTCT 240
QY 496 CCTCATTTTTTGGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCAGT 555
Db 241 CCTCATTTTTTGGGGGTGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCAGT 300
QY 556 CCTTCTGCCCTGCCGGGCGCGTTCGGGAGGCCCATG 592
Db 301 CCTTCTGCCCTGCCGGGCGCGTTCGGGAGGCCCATG 337

RESULT 11

ADI57209

ID ADI57209 standard; cDNA; 1321 BP.

XX ADI57209;

XX 22-APR-2004 (first entry)

XX Human PRL-3 encoding cDNA SEQ ID NO:29.

XX cell cycle arrest; CK2-specific siRNA molecule; short interfering RNA;

XX CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition;

XX Hbol-specific siRNA molecule; Hbol inhibition; cytostatic; gene therapy;

XX cancer; proliferative disorder; human; PRL-3; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 335..781

XX FT /*tag= a

XX FT /product= "PRL-3".

XX WO2004007754-A2.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-US022164.

XX 12-JUL-2002; 2002US-0395443P.

XX (RIGS-) RIGEL PHARM INC.

XX Hitoshi Y, Jenkins Y, Markovtsov V;

XX WPI; 2004-122975/12.

XX P-PSDB; ADI57210.

XX Identifying a compound that modulates cell cycle arrest, useful for
XX developing therapeutic reagents for treating cancer comprising contacting
XX a cell comprising a target polypeptide with the compound.

XX Claim 16; SEQ ID NO 29; 180pp; English.

XX The present invention describes a method for identifying a compound (C)
XX that modulates cell cycle arrest. The method comprises contacting a cell
XX comprising a target polypeptide with the compound (C), where the target
XX polypeptide encoded by the complement of a nucleic acid that hybridises
XX under stringent conditions to a nucleic acid encoding a polypeptide
XX having an amino acid sequence selected from 18 148-1408 amino acid
XX sequences (SEQ ID NO: 2-36, even numbers only). Also described: (i)
XX modulating cell cycle arrest in a subject; (2) a CK2-specific short
XX interfering RNA (siRNA) molecule comprising the sequence: (i)
XX AACATGATAGATCCAGCT, where the siRNA molecule is from 21-30 nucleotide
XX base pairs in length; (3) inhibiting expression of a CK2 gene in a cell;
XX (4) a PIM1-specific siRNA molecule comprising the sequence: (ii)
XX AAATCCGAGTGAAGTCTGC, where the siRNA molecule is from 21-30 nucleotide
XX base pairs in length; (5) inhibiting expression of a PIM1 gene in a cell;
XX (6) an Hbol-specific siRNA molecule comprising the sequence: (iii)
XX AACTGAGCAAGTGGTTGATT, where the siRNA molecule is from 21-30 nucleotide

PD 25-DEC-2003.
XX
PF 20-JUN-2002; 2002US-00177554.
XX
PR 20-JUN-2002; 2002US-00177554.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Zhang H;
XX
DR WPI: 2004-070585/07.
DR P-PSDB; ADI28335.
XX
XX New antisense oligonucleotide, comprising a sequence targeted to a
PT nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
PT -3), useful for preparing a composition for treating hyperproliferative
PT disorders, e.g., cancer.
XX
XX Example 15; SEQ ID NO 18; 77pp; English.
PS
XX The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
CC phosphatase type IVA member 3 (PRL-3), that specifically hybridizes with
CC the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
CC an antisense oligonucleotide (AO). Also included are a composition
CC comprising the compound and a carrier or diluent, inhibiting the
CC expression of PRL-3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with PRL-3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer (e.g. colorectal cancer), diabetes,
CC reduced glucose tolerance, insulin resistance and obesity. The present
CC sequence is a Human PRL3 target cDNA sequence.
XX
SQ Sequence 1396 BP; 281 A; 409 C; 400 G; 306 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1396;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTACTTTGGTTGGTTG 315
Db 1 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTACTTTGGTTGGTTG 60

QY 316 GGGGGGGCGGCGGCTGTTTGTCTTTTCTTTTAAAGAGTTGGTTTCTTTTAA 375
Db 61 GGGGGGGCGGCGGCTGTTTGTCTTTTCTTTTAAAGAGTTGGTTTCTTTTAA 120

QY 376 TTATCCAAACAGTGGGAGCTTCTCTCCCAAGTATTTGCAATATTTGTGCG 435
Db 121 TTATCCAAACAGTGGGAGCTTCTCTCCCAAGTATTTGCAATATTTGTGCG 180

QY 436 GGGTATCGGCGGCTGTTTAAATCTCGTTCTCTTGGACAGCAGGATCTCGTTCT 495
Db 181 GGGTATCGGCGGCTGTTTAAATCTCGTTCTCTTGGACAGCAGGATCTCGTTCT 240

QY 496 CCTCATTTTTTGGGGGTGTGGGAGCTTCTCAGTGTGTCCCGAGCTTCTCGAGT 555
Db 241 CCTCATTTTTTGGGGGTGTGGGAGCTTCTCAGTGTGTCCCGAGCTTCTCGAGT 300

QY 556 CCCTTCTGCCCTGCCGGGCGGCTGGGAGGCGGCATG 592
Db 301 CCCTTCTGCCCTGCCGGGCGGCTGGGAGGCGGCATG 337

RESULT 14
ADN75973
ID ADN75973 standard; DNA; 1396 BP.
XX
AC ADN75973;
XX 01-JUL-2004 (first entry)
DT
XX

DE Human signal transduction-associated DNA SEQ ID 798.
XX small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ds;
KW gene.
XX
XX Homo sapiens.
OS
XX WO2004016735-A2.
XX
XX 26-FEB-2004.
PD
XX 23-MAY-2003; 2003WO-US016632.
XX
PF 23-MAY-2003; 2002US-0383249P.
XX
PR 14-APR-2003; 2003US-0462942P.
XX
XX (CEPT-) CEPTOR INC.
XX (COLD-) COLD SPRING HARBOR LAB.
PA
XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
XX WPI: 2004-203773/19.
XX P-PSDB; ADN75974.
DR
DR New isolated small interfering RNA (siRNA) polynucleotide useful for
XX treating diseases with aberrant activity of the protein tyrosine
XX phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
PT
XX Disclosure; SEQ ID NO 798; 392pp; English.
XX
XX This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytostatic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 1396 BP; 281 A; 409 C; 400 G; 306 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1396;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTACTTTGGTTGGTTG 315
Db 1 TGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTACTTTGGTTGGTTG 60

QY 316 GGGGGGGCGGCGGCTGTTTGTCTTTTCTTTTAAAGAGTTGGTTTCTTTTAA 375
Db 61 GGGGGGGCGGCGGCTGTTTGTCTTTTCTTTTAAAGAGTTGGTTTCTTTTAA 120

QY 376 TTATCCAAACAGTGGGAGCTTCTCTCCCAAGTATTTGCAATATTTGTGCG 435
Db 121 TTATCCAAACAGTGGGAGCTTCTCTCCCAAGTATTTGCAATATTTGTGCG 180

QY 436 GGGTATCGGCGGCTGTTTAAATCTCGTTCTCTTGGACAGCAGGATCTCGTTCT 495
Db 181 GGGTATCGGCGGCTGTTTAAATCTCGTTCTCTTGGACAGCAGGATCTCGTTCT 240

QY 496 CCTCATTTTTTGGGGGTGTGGGAGCTTCTCAGTGTGTCCCGAGCTTCTCGAGT 555
Db 241 CCTCATTTTTTGGGGGTGTGGGAGCTTCTCAGTGTGTCCCGAGCTTCTCGAGT 300

QY 556 CCCTTCTGCCCTGCCGGGCGGCTGGGAGGCGGCATG 592
XX

Db 301 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCCCATG* 337

RESULT 15

ADP20802
ID ADP20802 standard; DNA; 1396 BP.

DT 09-SEP-2004 (first entry)

DE Human protein tyrosine phosphatase type IVA (Prl-3) gene.

ds; gene, metabolic; anorectic; antilipemic; cardiatic; osteopathic; antarthritic; antiinflammatory; cytostatic; gene therapy; Protein tyrosine phosphatase; metabolic disease; metabolic syndrome; obesity; diabetes; eating disorder; cachexia; hypertension; coronary heart disease; hypercholesterolemia; dyslipidemia; osteoarthritis; gallstones; liver fibrosis; transgenic animal.

OS Homo sapiens.

PN WO2004050117-A1.

17-JUN-2004.

PF 03-DEC-2003; 2003WO-EP013655.

PR 03-DEC-2002; 2002EP-00026921.

PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.

PI Meise M, Eulenberg K, Nguyen T, Tsetsenis T:

WPI: 2004-450615/42.

DR P-PSDB; ADP20803.

New pharmaceutical composition comprising a PRL-1 homologous protein or nucleic acid, and carriers, diluents or/and additives, useful for treating obesity, hyperlipidemia, osteoarthritis, cell masses.

PS Disclosure; SEQ ID NO 9; 89pp; English.

The invention relates to a pharmaceutical composition comprising a PRL-1 homologous protein or/and its functional fragment, a nucleic acid molecule encoding the protein, and/or a modulator/effector of the nucleic acid molecule or protein, and carriers, diluents or/and additives. The composition is useful for the manufacture of an agent for detecting or/and verifying for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity or/and diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, gallstones, or liver fibrosis, in cells, cell masses, organs and/or subjects in vivo or in vitro. The nucleic acid molecule and polypeptide are useful for the manufacture of a medicament for the treatment of obesity, diabetes, or/and metabolic syndrome for controlling the function of a gene or/and a gene product, which is influenced or/and modified by a PRL-1 homologous polypeptide, for identifying substances capable of interacting with a PRL-1 homologous polypeptide, and for the production of a non-human transgenic animal which over- or under-expresses the PRL-1. This sequence corresponds to the human protein tyrosine phosphatase type IVA member 3 i.e. Prl-3 gene.

Sequence 1396 BP; 281 A; 409 C; 400 G; 306 T; 0 U; 0 Other;

Query Match

Qy 256 TGA CTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTG 315
|||||
Dd 1 TGA CTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTG 60
|||||

GenCore version 5.1.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:13 ; Search time 736 Seconds
(without alignments)
6651.456 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctataggcagcggtgctg.....gccgcggagcgcccatg 592

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	592	100.0	592	7	US-10-624-670-1
2	557	94.1	1692	9	US-10-491-467-77
3	557	94.1	2181	8	US-10-723-860-4943
4	557	94.1	2850	3	US-09-918-715-247
5	557	94.1	2850	8	US-10-474-794-247
6	557	94.1	2850	9	US-10-979-159-247
7	555	93.8	909	6	US-10-177-554-19
8	551	93.1	986	7	US-10-624-670-2
9	410.6	69.4	1859	9	US-10-491-467-78
10	337	56.9	1321	6	US-10-177-554-4
11	337	56.9	1321	7	US-10-620-052A-29
12	337	56.9	1396	6	US-10-177-554-18
13	337	56.9	1396	7	US-10-444-795B-798
14	337	56.9	1396	10	US-11-060-756-2935
15	337	56.9	1396	10	US-11-060-756-7207
16	310	52.4	982	6	US-10-305-720-993
17	274.4	46.4	671	6	US-10-177-554-20
18	240	40.5	462	8	US-10-723-860-203
19	240	40.5	1006	6	US-10-177-554-239
20	221	37.3	773	6	US-10-277-161-71
21	139	23.5	1678	6	US-10-177-554-99
22	131.4	22.2	3222	6	US-10-177-554-11
23	58	9.8	396	7	US-10-021-323-17801

24	57	9.6	521	8	US-10-425-115-28564	Sequence 28564, A
25	55.2	9.3	683	8	US-10-425-115-92182	Sequence 92182, A
26	52.8	8.9	363	7	US-10-021-323-270	Sequence 270, App
27	52.8	8.9	1260	8	US-10-363-345A-3493	Sequence 3493, Ap
28	52.8	8.9	1260	8	US-10-363-345A-3494	Sequence 3494, Ap
29	52.8	8.9	1260	9	US-10-363-483A-3493	Sequence 3493, Ap
30	52.8	8.9	1260	9	US-10-363-483A-3494	Sequence 3494, Ap
31	52.4	8.9	444	7	US-10-424-599-85480	Sequence 85480, A
32	52.2	8.8	374	7	US-10-424-599-4878	Sequence 4878, Ap
33	52	8.8	7758	6	US-10-311-455-1076	Sequence 1076, Ap
34	51.2	8.6	192	7	US-10-021-323-5189	Sequence 5189, Ap
35	51	8.6	629	6	US-10-125-968-78	Sequence 78, Appl
36	50.8	8.6	7698	6	US-10-311-455-1673	Sequence 1673, Ap
37	50.6	8.5	369	8	US-10-425-115-162538	Sequence 162538, A
38	50.4	8.5	1025	8	US-10-363-345A-12421	Sequence 12421, A
39	50.4	8.5	1025	8	US-10-363-345A-12422	Sequence 12422, A
40	50.4	8.5	1025	9	US-10-363-483A-12421	Sequence 12421, A
41	50.4	8.5	1025	9	US-10-363-483A-12422	Sequence 12422, A
42	49.2	8.3	509	8	US-10-363-345A-5391	Sequence 5391, Ap
43	49.2	8.3	509	8	US-10-363-345A-5392	Sequence 5392, Ap
44	49.2	8.3	509	9	US-10-363-483A-5391	Sequence 5391, Ap
45	49.2	8.3	509	9	US-10-363-483A-5392	Sequence 5392, Ap

ALIGNMENTS

RESULT 1
US-10-624-670-1
; Sequence 1, Application US/10624670
; Publication No. US20040126785A1
; GENERAL INFORMATION:
; APPLICANT: Yuanho Li
; APPLICANT: De-Chao Yu
; TITLE OF INVENTION: Metastatic Colon Cancer Specific
; TITLE OF INVENTION: Promoter and Uses Thereof
; FILE REFERENCE: CELL-024
; CURRENT APPLICATION NUMBER: US/10/624,670
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/397,859
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-670-1

Query Match	100.0%	Score 592;	DB 7;	Length 592;
Best Local Similarity	100.0%	Pred. No. 2.8e-154;		
Matches 592;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTATAGGCGACGCGTGTGTCGACGCGCGCGGTGTGTTGAGTTGAGTTCAAGTTCA	60	
Db	1	CTATAGGCGACGCGTGTGTCGACGCGCGCGGTGTGTTGAGTTGAGTTCAAGTTCA	60	
Qy	61	TTCTTCTCTCGCCCTTGGGGCTTGGGGCCCACTCTGAGTGAAGGGGCTCTGCCC	120	
Db	61	TTCTTCTCTCGCCCTTGGGGCTTGGGGCCCACTCTGAGTGAAGGGGCTCTGCCC	120	
Qy	121	ATCCACCAATGTGAGAGGCGCGCCCGGTGTGGGGTCCAGCTCTGGACACCTGCTTGGCG	180	
Db	121	ATCCACCAATGTGAGAGGCGCGCCCGGTGTGGGGTCCAGCTCTGGACACCTGCTTGGCG	180	
Qy	181	CGCGGTTCACTTTGAGTTTAAAGTTTCTTGTGAGCTTTTGTGTTTCTTTT	240	
Db	181	CGCGGTTCACTTTGAGTTTAAAGTTTCTTGTGAGCTTTTGTGTTTCTTTT	240	
Qy	241	TTTTTGGCTTTTATGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTT	300	
Db	241	TTTTTGGCTTTTATGACTATCCAGCTCTGAGACGCGGAGTTGGAGTTGCCGCTTT	300	


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QY 96 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 155
DB 376 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 435
QY 156 GTCCAGCTCTGACACTGTCTGGCGCGGGTTCACCTTTGAGTTTTTAAGTTTTCTTTGC 215
DB 436 GTCCAGCTCTGACACTGTCTGGCGCGGGTTCACCTTTGAGTTTTTAAGTTTTCTTTGC 495
QY 216 TGAGCTTTTGGTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 275
DB 496 TGAGCTTTTGGTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 555
QY 276 ACGGAGTTTGGAGTTGCCCGCTTACTTTTGGTGGGCGGGCGGGCGGGCTGTTT 335
DB 556 ACGGAGTTTGGAGTTGCCCGCTTACTTTTGGTGGGCGGGCGGGCGGGCTGTTT 615
QY 336 TGTCTCTTTCTTTTAAAGAGTTGGGTTTCTTTTAAATTAATTAATTAATTAATTAATTAAT 395
DB 616 TGTCTCTTTCTTTTAAAGAGTTGGGTTTCTTTTAAATTAATTAATTAATTAATTAATTAAT 455
QY 396 TTCCTCCCCACACCAAGTATTTGCAATATTTTGTGGGGGTATGGGGGTGGGTTTTT 455
DB 676 TTCCTCCCCACACCAAGTATTTGCAATATTTTGTGGGGGTATGGGGGTGGGTTTTT 735
QY 456 AAATCTCGTTTCTCTTGGACAAGCAGGGATCTCGTTCTCTCTCAATTTTGGGGGTGTG 515
DB 736 AAATCTCGTTTCTCTTGGACAAGCAGGGATCTCGTTCTCTCTCAATTTTGGGGGTGTG 795
QY 516 TGGGAGCTTCTCAGTGTGTGCCAGCCTTCTCTGCACTCCCTTCTGCCCTGCCGGGCC 575
DB 796 TGGGAGCTTCTCAGTGTGTGCCAGCCTTCTCTGCACTCCCTTCTGCCCTGCCGGGCC 855
QY 576 CGTCGGAGGGGCCCATG 592
DB 856 CGTCGGAGGGGCCCATG 872
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RESULT 4

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US-09-918-715-247
; Sequence 247, Application US/09918715
; Publication No. US20030017157A1
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GENERAL INFORMATION:

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; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 247
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match

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Best Local Similarity 94.1%; Score 557; DB 3; Length 2850;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 36 CTGAGTTGGTTCAAGTTCATTTCTTCTCTGGCCCTTGGGGCTTGGGGCCCAACC 95
DB 345 CTGAGTTGGTTCAAGTTCATTTCTTCTCTGGCCCTTGGGGCTTGGGGCCCAACC 404
QY 96 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 155
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DB 405 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 464
QY 156 GTCCAGCTCTGACACTGTCTGGCGCGGGTTCACCTTTGAGTTTTTAAGTTTTCTTTGC 215
DB 465 GTCCAGCTCTGACACTGTCTGGCGCGGGTTCACCTTTGAGTTTTTAAGTTTTCTTTGC 524
QY 216 TGAGCTTTTGGTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 275
DB 525 TGAGCTTTTGGTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 584
QY 276 ACGGAGTTTGGAGTTGCCCGCTTACTTTTGGTGGGCGGGCGGGCGGGCTGTTT 335
DB 585 ACGGAGTTTGGAGTTGCCCGCTTACTTTTGGTGGGCGGGCGGGCGGGCTGTTT 644
QY 336 TGTCTCTTTCTTTTAAAGAGTTGGGTTTTCTTTTAAATTAATTAATTAATTAATTAATTAAT 395
DB 645 TGTCTCTTTCTTTTAAAGAGTTGGGTTTTCTTTTAAATTAATTAATTAATTAATTAATTAAT 704
QY 396 TTCCTCCCCACACCAAGTATTTGCAATATTTTGTGGGGGTATGGGGGTGGGTTTTT 455
DB 705 TTCCTCCCCACACCAAGTATTTGCAATATTTTGTGGGGGTATGGGGGTGGGTTTTT 764
QY 456 AAATCTCGTTTCTCTTGGACAAGCAGGGATCTCGTTCTCTCTCAATTTTGGGGGTGTG 515
DB 765 AAATCTCGTTTCTCTTGGACAAGCAGGGATCTCGTTCTCTCTCAATTTTGGGGGTGTG 824
QY 516 TGGGAGCTTCTCAGTGTGTGCCAGCCTTCTCTGCACTCCCTTCTGCCCTGCCGGGCC 575
DB 825 TGGGAGCTTCTCAGTGTGTGCCAGCCTTCTCTGCACTCCCTTCTGCCCTGCCGGGCC 884
QY 576 CGTCGGAGGGGCCCATG 592
DB 885 CGTCGGAGGGGCCCATG 901
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RESULT 5

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US-10-474-794-247
; Sequence 247, Application US/10474794
; Publication No. US20040213793A1
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GENERAL INFORMATION:

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; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match

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Best Local Similarity 94.1%; Score 557; DB 8; Length 2850;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 36 CTGAGTTGGTTCAAGTTCATTTCTTCTCTGGCCCTTGGGGCTTGGGGCCCAACC 95
DB 345 CTGAGTTGGTTCAAGTTCATTTCTTCTCTGGCCCTTGGGGCTTGGGGCCCAACC 404
QY 96 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 155
DB 405 TCTGAGTGAAGGGGGCTGTCTGCCATCCACCAATGTGAGAGGGGCGCCCGGTGTGGG 464
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Db 1 TGGCGGCGGGTTCACCTTGAGTTTGGAGTCGTCTTGTGAGCTTTTGTGGTGTCT 60
Qy 236 TTTTATTTTGGCTCTTATGATCTATCCAGCTCTGAGAGCGGGATTTGGAGTTCGCC 295
Db 61 TTTTATTTTGGCTCTTATGATCTATCCAGCTCTGAGAGCGGGATTTGGAGTTCGCC 120
Qy 296 GCTTTACTTTGGTGGTGGGGGGCGGGGCTGTTTGTTCCTTTTCTTTTAAAG 355
Db 121 GCTTTACTTTGGTGGTGGGGGGCGGGGCTGTTTGTTCCTTTTCTTTTAAAG 180
Qy 356 AGTTGGGTTTCTTTTAAATATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGT 415
Db 181 AGTTGGGTTTCTTTTAAATATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGT 240
Qy 416 ATTTGACAAATATTTGGGGGATGCGGGGATGCGGGGTTTAAATCTGTTTCTTCGGAC 475
Db 241 ATTTGACAAATATTTGGGGGATGCGGGGATGCGGGGTTTAAATCTGTTTCTTCGGAC 300
Qy 476 AAGCACAGGATCTCGTTCTCTCTCAATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTG 535
Db 301 AAGCACAGGATCTCGTTCTCTCTCAATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTG 360
Qy 536 TCCCCAGCTTCTCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 592
Db 361 TCCCCAGCTTCTCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417

RESULT 10

US-10-177-554-4
; Sequence 4, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 4
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (335)...(781)
US-10-177-554-4

Query Match 56.9%; Score 337; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 256 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCTTTACTTTGGTGGGTG 315
Db 1 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCTTTACTTTGGTGGGTG 60
Qy 316 GGGGGGCGGGCTGTTTGTTCCTTTTAAAGTGGGTTTCTTTTAA 375
Db 61 GGGGGGCGGGCTGTTTGTTCCTTTTAAAGTGGGTTTCTTTTAA 120
Qy 376 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 435
Db 121 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 180
Qy 436 GGGTATGGGGTGGGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 495
Db 181 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 180
Qy 496 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTGCAAGCAGGAGTCTCGTTCT 495
Db 181 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTGCAAGCAGGAGTCTCGTTCT 240
Qy 496 CCTCATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTGCCAGCTTCTCTGAGT 555
Db 241 CCTCATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTGCCAGCTTCTCTGAGT 300

Qy 556 CCCTTCTGCCCTGCCGGGCGCGCTCGGAGGCGCCATG 592
Db 301 CCCTTCTGCCCTGCCGGGCGCGCTCGGAGGCGCCATG 337

RESULT 11

US-10-620-052A-29
; Sequence 29, Application US/10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Markovtsov, Vadim
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Cellular Proliferation
; FILE REFERENCE: 021044-004010US
; CURRENT APPLICATION NUMBER: US/10/620,052A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/395,443
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: potentially prenylated protein tyrosine
; OTHER INFORMATION: phosphatase (PRL-3), protein tyrosine phosphatase
; OTHER INFORMATION: type IVA, member 3, isoform 2, transcript variant
; OTHER INFORMATION: 2 (PTP4A3)
US-10-620-052A-29

Query Match 56.9%; Score 337; DB 7; Length 1321;
Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 256 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCTTTACTTTGGTGGGTG 315
Db 1 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCTTTACTTTGGTGGGTG 60
Qy 316 GGGGGGCGGGCTGTTTGTTCCTTTTAAAGTGGGTTTCTTTTAA 375
Db 61 GGGGGGCGGGCTGTTTGTTCCTTTTAAAGTGGGTTTCTTTTAA 120
Qy 376 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 435
Db 121 TTATCCAAACAGTGGGAGCTTCTCCCCACACCCAAAGTATTTGCAATATTTGCG 180
Qy 436 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGACACAGGAGTCTCGTTCT 495
Db 181 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGACACAGGAGTCTCGTTCT 240
Qy 496 CCTCATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTGCCAGCTTCTCTGAGT 555
Db 241 CCTCATTTTGGGGGTGTGGGAGCTTCTCAGTCTGTGCCAGCTTCTCTGAGT 300
Qy 556 CCCTTCTGCCCTGCCGGGCGCGCTCGGAGGCGCCATG 592
Db 301 CCCTTCTGCCCTGCCGGGCGCGCTCGGAGGCGCCATG 337

RESULT 12

US-10-177-554-18
; Sequence 18, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554

; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 18
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (335)...(856)
US-10-177-554-18

Query Match 56.9%; Score 337; DB 6; Length 1396;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 315
DB 1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 60
QY 316 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 375
DB 61 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 120
QY 376 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 435
DB 121 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 180
QY 436 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 495
DB 181 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 240
QY 496 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 555
DB 241 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 300
QY 556 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 592
DB 301 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 337

RESULT 13
US-10-444-795B-798
; Sequence 798, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; FILE REFERENCE: 200125 449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-444-795B-798

Query Match 56.9%; Score 337; DB 7; Length 1396;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 315
DB 1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 60
QY 316 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 375
DB 61 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 120

QY 376 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 435
DB 121 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 180
QY 436 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 495
DB 181 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 240
QY 496 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 555
DB 241 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 300
QY 556 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 592
DB 301 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 337

RESULT 14
US-11-060-756-2935
; Sequence 2935, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2935

Query Match 56.9%; Score 337; DB 10; Length 1396;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 315
DB 1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCGCTTACTTTGTTGGGTTG 60
QY 316 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 375
DB 61 GGGGGGGGGGGGGGCTTTTGTCTCTTTTAAAGAGTTGGGTTTCTTTTTTAA 120
QY 376 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 435
DB 121 TTATCCAAACAGTGGGACGCTTCTCCCCCACACCAAGTATTGCAATATTGTGCG 180
QY 436 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 495
DB 181 GGGTATGGGGTGGGTTTAAATCTCGTTTCTTTGGAACAAGCAGGAGTCTCGTTCT 240
QY 496 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 555
DB 241 CCTCATTTTGGGGTGTGGGACTTCTCAGTCTGTCGCCAGCCTTCTCTGCACT 300
QY 556 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 592
DB 301 CCTTCTGCCCTGCCGGCCCGTGGGAGGCCCATG 337

RESULT 15
US-11-060-756-7207
; Sequence 7207, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; TITLE OF INVENTION: Target Genes

; FILE REFERENCE: AM101083 (031896-042000)

; CURRENT APPLICATION NUMBER: US/11/060,756

; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7207

; LENGTH: 1396

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-060-756-7207

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Query Match      56.9%; Score 337; DB 10; Length 1396;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 315
Db      1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 60

Qy      316 GGGGGGGGGGGGGCTGTTTGTTCCTTTCTTTTAAAGAGTTGGGTTTCTTTTAA 375
Db      61 GGGGGGGGGGGGGCTGTTTGTTCCTTTCTTTTAAAGAGTTGGGTTTCTTTTAA 120

Qy      376 TTATCCAAACAGTGGGAGCTTCTCCCAACACCAAGTATTTGCACAATATTTGTGG 435
Db      121 TTATCCAAACAGTGGGAGCTTCTCCCAACACCAAGTATTTGCACAATATTTGTGG 180

Qy      436 GGGTATGGGGTGGGTTTTTAAATCTCGTTTCTTTGGACAAGCACAGGGATCTCGTTCT 495
Db      181 GGGTATGGGGTGGGTTTTTAAATCTCGTTTCTTTGGACAAGCACAGGGATCTCGTTCT 240

Qy      496 CCTCATTTTTTGGGGGTGTGTGGGAGCTTCTCAGGTGTGTCTCCAGGCTTCTCTGCAGT 555
Db      241 CCTCATTTTTTGGGGGTGTGTGGGAGCTTCTCAGGTGTGTCTCCAGGCTTCTCTGCAGT 300

Qy      556 CCCTTCTGCCCTGCCGGCCCGTCGGGAGGCCCATG 592
Db      301 CCCTTCTGCCCTGCCGGCCCGTCGGGAGGCCCATG 337
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Search completed: April 3, 2006, 05:55:10
Job time : 738 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:40:07 ; Search time 1439 Seconds
(without alignments)
1642.707 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctatgggcacgcgtggtcg.....gcccgtagggagcgccatg 592

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /SIDSS/ptodata/1/pubpna/US08 NEW PUB.seq.*
- 2: /SIDSS/ptodata/1/pubpna/US06 NEW PUB.seq.*
- 3: /SIDSS/ptodata/1/pubpna/US07 NEW PUB.seq.*
- 4: /SIDSS/ptodata/1/pubpna/PTCT_NEW PUB.seq.*
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- 13: /SIDSS/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 14: /SIDSS/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 15: /SIDSS/ptodata/1/pubpna/US60_NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	46.6	7.9	5562	US-10-240-708-63
2	45.6	7.7	6156	US-10-240-708-60
3	45.2	7.6	22118	US-11-082-154A-18
4	43	7.3	995	US-10-301-480-611851
5	43	7.3	995	US-10-301-480-1225260
6	43	7.3	137454	US-10-330-773-365
7	42.6	7.2	7001	US-11-011-332A-103
8	42.6	7.2	8252	US-11-011-332A-158
9	42.4	7.2	8467	US-11-011-332A-96
10	42.2	7.1	3641	US-11-102-026A-181
11	42	7.1	4453	US-11-011-332A-98
12	41.6	7.0	587	US-09-925-065A-760778
13	41.6	7.0	587	US-09-925-065A-760779
14	41.6	7.0	59002	US-10-330-773-966
15	41.4	7.0	614	US-09-925-065A-36845
16	41.4	7.0	614	US-10-301-480-138083
17	41.4	7.0	614	US-10-301-480-751492
18	41.4	7.0	28536	US-11-011-332A-156

19	41.2	7.0	19233	8	US-10-240-708-45	Sequence 45, Appl
20	41	6.9	6499	14	US-11-011-332A-91	Sequence 91, Appl
21	40.8	6.9	635	9	US-10-920-625-60	Sequence 60, Appl
22	40.8	6.9	5455	8	US-10-240-708-34	Sequence 34, Appl
23	40.8	6.9	10490	14	US-11-011-332A-101	Sequence 101, Appl
24	40.4	6.8	210920	9	US-10-330-773-99	Sequence 99, Appl
25	40.2	6.8	614	6	US-09-925-065A-36846	Sequence 36846, A
26	40.2	6.8	614	6	US-09-925-065A-36847	Sequence 36847, A
27	40.2	6.8	614	9	US-10-301-480-138084	Sequence 138084, A
28	40.2	6.8	614	9	US-10-301-480-138085	Sequence 138085, A
29	40.2	6.8	614	10	US-10-301-480-751493	Sequence 751493, A
30	40.2	6.8	614	10	US-10-301-480-751494	Sequence 751494, A
31	40.2	6.8	666	6	US-09-925-065A-534678	Sequence 534678, A
32	40.2	6.8	892	10	US-10-301-480-539021	Sequence 539021, A
33	40.2	6.8	892	10	US-10-301-480-1152430	Sequence 1152430, A
34	40	6.8	800	9	US-10-920-625-61	Sequence 61, Appl
35	39.8	6.7	5666	8	US-10-240-708-29	Sequence 29, Appl
36	39.6	6.7	6583	8	US-10-240-708-26	Sequence 26, Appl
37	39.2	6.6	411	8	US-10-927-641-30	Sequence 30, Appl
38	39.2	6.6	2791	11	US-11-192-123-1	Sequence 1, Appl
39	39.2	6.6	8467	14	US-11-011-332A-97	Sequence 97, Appl
40	39.2	6.6	157224	14	US-11-112-908-51	Sequence 51, Appl
41	39.2	6.6	170189	14	US-11-112-908-50	Sequence 50, Appl
42	39	6.6	810	11	US-11-096-568A-9782	Sequence 9782, Appl
43	39	6.6	1031	11	US-11-174-413-66	Sequence 66, Appl
44	39	6.6	2240	11	US-11-166-234-6	Sequence 6, Appl
45	39	6.6	2344	9	US-10-920-625-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-10-240-708-63
; Sequence 63, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 63
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-63

Query Match	7.9%	Score 46.6;	DB 8;	Length 5562;
Best Local Similarity	56.1%	Pred. No. 1.2;		
Mismatches	88;	Conservative	0;	Mismatches 69;
Indels	0;	Gaps	0;	
217	GAGCTTTTGGTGTCTTTTATTTTTCCTCTTATGACTATCCAGCTCTCAGAGA	276		
3732	GATTTTGTCTTTTATTTTTCCTCTTATGACTATCCAGCTCTCAGAGA	3791		
277	CGGAGTTTGGAGTTGCGCGCTTTACTTTGGTTGGTTGGGGGGGGCGGCGGCTGTTT	336		

Db 3792 GTTTATTTGGAGATTATTAGTATTAGTTGGTTTCGGGTGCGGGGTGTTTGT 3851
QY 337 GTTCCCTTTCTTTTAAAGATTGGGTTTCTTTT 373
Db 3852 TTTTATTTTATTTTATTTATGTCGTTTATATTT 3888

RESULT 2
US-10-240-708-60
; Sequence 60, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT FILING DATE: 2002-10-03
; PRIOR FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 60
; LENGTH: 6156
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-60

Query Match 7.7%; Score 45.6; DB 8; Length 6156;
Best Local Similarity 52.7%; Pred. No. 2;
Matches 99; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 192 TTTGAGTTTAAAGTTTCTTCTGCTGAGCTTTTGTGTTCTTTTATTTTGGCTC 251
Db 1453 TTTTATTTTATTTTATTTTATTTTGTAGTTTTCGTTATTTTCGTTATTTACGGCTC 1512
QY 252 TTTATGACTATCCAGTCTGAGACGGGAGTTGGAGTTGCCGCTTACTTTGGTGG 311
Db 1513 GGGTTTATTTAGTAGAGTGTATTGAGGAAGACGGAGATTTTATTTTATTTAGTAGGT 1572
QY 312 GTTGGGGGGCGCGCGGCTGTTTGTCTTTCTTTTCTTTTAAAGATTGGGTTTCTTTT 371
Db 1573 TGTCGCGGGAGCGCGGGTTTATCGTTTTCGTCGCTGTTTTCGTTTTCGTTTTCGTTT 1632
QY 372 TTAATTAT 379
Db 1633 TTTTATTT 1640

RESULT 3
US-11-082-154A-18
; Sequence 18, Application US/11082154A
; Publication No. US20060024820A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra

; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 17084-022003 (420C)
; CURRENT APPLICATION NUMBER: US/11/082,154A
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 10/161,403
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 22118
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X82564
; DATABASE ENTRY DATE: 1996-04-09
US-11-082-154A-18

Query Match 7.6%; Score 45.2; DB 14; Length 22118;
Best Local Similarity 52.7%; Pred. No. 3.3;
Matches 98; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 192 TTTGAGTTTAAAGTTTCTTCTGCTGAGCTTTTGTGTTCTTTTATTTTGGCTC 251
Db 19801 TTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 19860
QY 252 TTTATGACTATCCAGTCTGAGACGGGAGTTGGAGTTGCCGCTTACTTTGGTGG 311
Db 19861 TTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 19920
QY 312 GTTGGGGGGCGCGCGGCTGTTTGTCTTTCTTTCTTTTAAAGATTGGGTTTCTTTT 371
Db 19921 GTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 19980
QY 372 TTAATT 377
Db 19981 TTTGTTT 19986

RESULT 4
US-10-301-480-611851
; Sequence 611851, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 611851
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-611851

Query Match 7.3%; Score 43; DB 10; Length 995;
Best Local Similarity 51.9%; Pred. No. 5.1;
Matches 97; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 187 TTCACCTTTGAGTTTTTAAAGTTTCTTTGCTGAGCTTTTGGTGTGTTCTTTTATTTTT 246
Db 430 TTCAAATGACTAATTTTGCATTCGTCTTCTTTGTAATGAAGTTTTTTTTTTTTTTT 489

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QY 247 GCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTCGCCGCTTTACTTTG 306
D 490 TTTTCTTTTCTCTCTTTAATGATCATAGACATGACATTCCTTTAGTCAATACAGTTA 549
QY 307 GTTGGTTGGGGGGGGGGGGGCTTTTGTCTCTTTTCTTTTAAAGATGGGTTT 366
D 550 ATTGTGTGTGAGTGTGCGTGCATGTGTGACACGGTTCCTTTTGAAGGATGGTTG 609
QY 367 CTTTTTT 373
D 610 CTGATCT 616

RESULT 5
US-10-301-480-1225260
; Sequence 1225260, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/301,480
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1225260
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1225260

Query Match
Best Local Similarity 7.3%; Score 43; DB 10; Length 995;
Matches 97; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 187 TTCATTTGAGTTTAAAGTTTCTTTGTCGAGCTTTTGGTGTCTTTTATTTT 246
D 430 TTTCAAAATGACTAATTTTGCATCTCTGCTTTTGTAAATGAAGTTT 489
QY 247 GCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTCGCCGCTTTACTTTG 306
D 490 TTTTCTTTTCTCTTTTAAATGATCATAGACATGACATTCCTTTAGTCAATACAGTTA 549
QY 307 GTTGGTTGGGGGGGGGGGGGCTTTTGTCTCTTTTCTTTTAAAGATGGGTTT 366
D 550 ATTGTGTGTGAGTGTGCGTGCATGTGTGACACGGGTTCTTTTGAAGGATGGTTG 609
QY 367 CTTTTTT 373
D 610 CTGATCT 616

RESULT 6
US-10-330-773-365/c
; Sequence 365, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 137454
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TYPE: DNA
ORGANISM: Mus musculus
US-10-330-773-365

Query Match
Best Local Similarity 7.3%; Score 43; DB 9; Length 137454;
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 61 TCTTCTCTGCGCCCTTGGGGGCTTGGGGCCCACTCTGAGTGAAGGGGGCTGTCTGCC 120
D 115071 TCTCTGTATAGCCCTGCTGCTGAGCTCCTTTGTAGACAGGCTGGCTCGAATC 115012
QY 121 ATCCACCAATGTGAGAGAGGGGGCCCCCGGTGTGGGTCCAGCTCTGGACACTGCTTGGCG 180
D 115011 AGAAATCCACCTGCTCTGCTCCCGAGTGTCTGGGATTAAGGCATGCCACCATGCC 114952
QY 181 GCGGGTTCACTTTGAGTTTAAAGTTTCTTTGCTGAGCTTTTGGTGTCTTTT 240
D 114951 GCGTCTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 114892
QY 241 TTTTGTGCTCTTTA 255
D 114891 AATTTATTTT 114877

RESULT 7
US-11-011-332A-103
; Sequence 103, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimmrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dimo
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwöpe, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR S
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
```

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; SEQ ID NO 103
; LENGTH: 7001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-103

Query Match          7.2%; Score 42.6; DB 14; Length 7001;
Best Local Similarity 52.5%; Pred. No. 9.7; Mismatches 0; Gaps 0;
Matches 93; Conservative 0; Indels 84; Indels 0; Gaps 0;

QY 199 TTTTAAAGTTTCTTGGTGGAGCTTTTGGTGTCTTTTATTTTGGCTCTTTATGA 258
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 6296 TTTTGGGTATTTGGGATGATGGTTTGTGTTGTTGATATGTTTGTGTTTTTTT 6355

QY 259 CTATCCAGCTCTGAGAGACGGAGTTGGAGTGGCGCTTACTTTGGTGGTTGGG 318
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 6356 TTATTAGATTTTATAGATTTTATTTTATTTTATTTTATTTTATTTTATTTT 6415

QY 319 GGGCGGCGGGCTGTTTGTCTCTTTCTTTTAAAGAGTTGGTCTTTCTTTTAA 375
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 6416 AGTTGGAGTGTAAAGTGTGATTTTGGTTTATTAATTTTGTGTTTGGTTTA 6472

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RESULT 8
US-11-011-332A-158
; Sequence 158, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimmrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dimo
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwöpe, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SU
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158

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; SEQ ID NO 158
; LENGTH: 8252
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-158

Query Match          7.2%; Score 42.6; DB 14; Length 8252;
Best Local Similarity 52.5%; Pred. No. 10; Mismatches 0; Gaps 0;
Matches 93; Conservative 0; Indels 84; Indels 0; Gaps 0;

QY 199 TTTTAAAGTTTCTTGGTGGAGCTTTTGGTGTCTTTTATTTTGGCTCTTTATGA 258
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 4335 TTTTGGGTATTTGGGATGATGGTTTGTGTTGTTGATATGTTTGTGTTTTTTT 4394

QY 259 CTATCCAGCTCTGAGAGACGGAGTTGGAGTGGCGCTTACTTTGGTGGTTGGG 318
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 4395 TTATTAGATTTTATAGATTTTATTTTATTTTATTTTATTTTATTTTATTTT 4454

QY 319 GGGCGGCGGGCTGTTTGTCTCTTTCTTTTAAAGAGTTGGTCTTTCTTTTAA 375
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 4455 AGTTGGAGTGTAAAGTGTGATTTTGGTTTATTAATTTTGTGTTTGGTTTA 4511

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RESULT 9
US-11-011-332A-96
; Sequence 96, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimmrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dimo
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwöpe, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SI
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158

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US-11-011-332A-98

Query Match 7.1%; Score 42; DB 14; Length 4453;
Best Local Similarity 49.5%; Pred. No. 12;
Matches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 160 AGCTCTGGACACGCTTGGCGCGCGGCTTCACCTTGGAGTTTAAAGTTTCTTTGCTGAG 219
DB 2010 AGTGGGAGCTGGTTATTGTGGGATTTTGTGTTGTTAGTTCTTTGTTGGTTG 2069
QY 220 CTTTGTGTTGTTCTTTTATTTTATTTTGGCTCTTTATGATATCCAGCTCTGAGACGG 279
DB 2070 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTAG 2129
QY 280 GAGTTTGGAGTCCCGCTTACTTTGGTTGGTTGGGTTGGGCGGCGGCTCTTTTGT 339
DB 2130 TGTGTTGATTTGTTATATGAGAGTTTCTGTTGGTGTGTTTGTGTTTGTGTTTGTGTTTGT 2189
QY 340 CTTTCTTTCTTTTAAAGAGTTGGGTTTCTTTTCTTTTAAAT 377
DB 2190 GTGAGTGAATTTAAAGTGAAGTGTGTTTCTTTGTTGATT 2227;

RESULT 12

US-09-925-065A-760778/c
; Sequence 760778, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 760778
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-760778

Query Match 7.0%; Score 41.6; DB 6; Length 587;
Best Local Similarity 53.0%; Pred. No. 9.3;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 198 TTTTAAAGTTTCTTTGCTGAGCTTTTGGTTGTTGTTGTTTATTTTGGCTCTTTATG 257
DB 171 TCTTCTATTTTCTTCTTATTTAGTAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 112
QY 258 ACTATCCAGCTCTGAGACGGAGTTGGAGTTGCCCGCTTTACTTTGTTGGTTGGGTTGG 317
DB 111 AAAACCCAACTTTGTTTCTTCAATTTAGTAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 52
QY 318 GGGGCGGCGGCTGTTTGTTCCTTTTCTTTTAAAGAGTTGGGTTT 365
DB 51 TTCTGCTCTGGTCTTTATTTCTTTCTTCTTATTAATTTGGGTTT 4

RESULT 13

US-09-925-065A-760779/c
; Sequence 760779, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 760779
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-760779

Query Match 7.0%; Score 41.6; DB 6; Length 587;
Best Local Similarity 53.0%; Pred. No. 9.3;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 198 TTTTAAAGTTTCTTTGCTGAGCTTTTGGTTGTTGTTGTTTATTTTGGCTCTTTATG 257
DB 171 TCTTCTATTTTCTTCTTATTTAGTAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 112
QY 258 ACTATCCAGCTCTGAGACGGAGTTGGAGTTGCCCGCTTTACTTTGTTGGTTGGGTTGG 317
DB 111 AAAACCCAACTTTGTTTCTTCAATTTAGTAGTATGTTTCTTAACTTCAATTCATTAT 52
QY 318 GGGGCGGCGGCTGTTTGTTCCTTTTCTTTTAAAGAGTTGGGTTT 365
DB 51 TTCTGCTCTGGTCTTTATTTCTTTCTTCTTATTAATTTGGGTTT 4

RESULT 14

US-10-330-773-966/c
; Sequence 966, Application US/10330773
; Publication No. US20060040262A1

GENERAL INFORMATION:

; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 966
; LENGTH: 59002
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (59002)

OTHER INFORMATION: n = A, T, C or G

US-10-330-773-966

Query Match 7.0%; Score 41.6; DB 9; Length 59002;
Best Local Similarity 54.6%; Pred. No. 26;
Matches 83; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 221 TTTTGTGTTGTTCTTTTATTTTGTGCTCTTTATGATATCCAGCTCTGAGACGGG 280
DB 9617 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT 9558

QY 281 AGTTGGAGTTGCCCGCTTTACTTTGGTTGGTTGGGGGGGGGGCGGCTTTTGTTC 340
Db 9557 GGTTCGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT 9498
QY 341 CTTTCTTTTTTAAGAGTTGGGTTTCTTTTT 372
Db 9497 GGTTCGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT 9466

RESULT 15
US-09-925-065A-36845/c
; Sequence 36845, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36845
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-36845

Query Match 7.0%; Score 41.4; DB 6; Length 614;
Best Local Similarity 53.5%; Pred. No. 10;
Matches 84; Conservative 1; Mismatches 72; Indels 0; Gaps 0;
QY 197 GTTTTAAAGTTTCTTGTGAGCTTTTGTGTTGTTGTTTATTTTGGCTCTTTAT 256
Db 364 GTCTTTTCTTTTCTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 305
QY 257 GACTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCGCTTACTTTGGTTGGTTGG 316
Db 304 GAGCTTGTCTGTCAACCAGGCTGAAGTGCAGTGGTCAATCTCTGCTCGCTCAAAAGT 245
QY 317 GGGGGGGGGGGCTGTGTTTGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 353
Db 244 TTGGAGGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTGA 208

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